

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:51:43 ; Search time 51 Seconds  
(without alignments)  
34.326 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKKRRQRRKPSADGHR 20

Scoring table:

OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 641544

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Issued Patents AA.\*

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- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	11	55.0	11	1	US-08-924-695A-54
5	11	55.0	11	2	US-09-208-966-2
6	11	55.0	11	2	US-09-296-089-37
7	11	55.0	11	2	US-09-837-863-2
8	11	55.0	11	2	US-09-660-742-1
9	11	55.0	11	2	US-09-434-345-2
10	11	55.0	11	2	US-09-632-287A-22
11	11	55.0	11	2	US-09-632-277A-4
12	11	55.0	11	2	US-09-632-033B-15
13	11	55.0	11	2	US-09-780-070-37
14	11	55.0	11	2	US-09-775-052A-2
15	11	55.0	11	2	US-09-911-842A-6
16	11	55.0	11	2	US-09-997-465B-2
17	11	55.0	11	2	US-10-083-889-17
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19	11	55.0	11	2	US-09-265-107-75
20	11	55.0	11	2	US-09-724-126A-16
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26	11	55.0	11	2	US-09-909-474D-5

Sequence 1899, Ap  
Sequence 21, Appl  
Sequence 3, Appl  
Sequence 13, Appl  
Sequence 18, Appl  
Sequence 5, Appl  
Sequence 24, Appl  
Sequence 47, Appl  
Sequence 47, Appl  
Sequence 47, Appl  
Sequence 50, Appl  
Sequence 46, Appl  
Sequence 173, App  
Sequence 289, App  
Sequence 4, Appl  
Sequence 10, Appl

27 11 55.0 11 2 US-09-667-365-1899  
28 11 55.0 11 2 US-09-653-182-21  
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30 11 55.0 11 2 US-09-895-593-13  
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32 11 55.0 11 3 US-10-117-766A-5  
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34 11 55.0 12 1 US-08-450-257-47  
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37 11 55.0 12 1 US-08-451-233-47  
38 11 55.0 12 1 US-08-450-236-47  
39 11 55.0 12 1 US-08-733-505A-50  
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41 11 55.0 12 2 US-09-254-126D-46  
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44 11 55.0 14 5 PCT-US95-06077-4  
45 11 55.0 14 5 PCT-US95-06077-10

#### ALIGNMENTS

RESULT 1  
US-09-656-121-14  
; Sequence 14, Application US/09656121  
; Patent No. 6706892  
; GENERAL INFORMATION:  
; APPLICANT: CONJUCHEM, INC.  
; APPLICANT: EZRIN, ALAN M.  
; APPLICANT: FLEISER, ANGELICA  
; APPLICANT: ROBITAILLE, MARTIN  
; APPLICANT: MILNER, PETER G.  
; APPLICANT: BRIDON, DOMINIQUE P.  
; TITLE OF INVENTION: PULMONARY DELIVERY FOR BIOCONJUGATION  
; FILE REFERENCE: REDC-1810  
; CURRENT APPLICATION NUMBER: US/09/656,121  
; CURRENT FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/152,681  
; PRIOR FILING DATE: 1999-09-07  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-656-121-14

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Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRK 12

Db 1 YGRKKRRQRRRK 12

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US-09-656-121-15  
; Sequence 15, Application US/09656121  
; Patent No. 6706892  
; GENERAL INFORMATION:  
; APPLICANT: CONJUCHEM, INC.  
; APPLICANT: EZRIN, ALAN M.  
; APPLICANT: FLEISER, ANGELICA  
; APPLICANT: ROBITAILLE, MARTIN  
; APPLICANT: MILNER, PETER G.  
; APPLICANT: BRIDON, DOMINIQUE P.  
; TITLE OF INVENTION: PULMONARY DELIVERY FOR BIOCONJUGATION

us-10-814-109-2.oligo.ra1

Fri Aug 25 11:24:28 2006

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; FILE REFERENCE: REDC-1810
; CURRENT APPLICATION NUMBER: US/09/656.121
; CURRENT FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/152,681
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-656-121-15

Query Match          60.0%; Score 12; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YGRKKRRQRRK 12

RESULT 3
US-08-706-741B-54
; Sequence 54, Application US/08706741B
; Patent No. 5955593
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,741B
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-6092
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-706-741B-54

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Best Local Similarity 100.0%; Pred. No. 0.00013;
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DB 1 YGRKKRRQRR 11

RESULT 5
US-09-208-966-2
; Sequence 2, Application US/09208966
; Patent No. 6221355
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48861/1742
; CURRENT APPLICATION NUMBER: US/09/208,966
; CURRENT FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/082,402
; EARLIER FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: 60/069,012
; EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-208-966-2

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DB 1 YGRKKRRQRR 11
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Qy 1 YGRKKRRQRRR 11  
Db 1 YGRKKRRQRRR 11

## RESULT 6

US-09-296-089-37  
; Sequence 37, Application US/09296089  
; Patent No. 6303576  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Byers, Stephen  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: BETA-CATENIN MEDIATED GENE EXPRESSION  
; FILE REFERENCE: 100086.411  
; CURRENT APPLICATION NUMBER: US/09/296,089  
; CURRENT FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-296-089-37

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Best Local Similarity 100.0%; Pred. No. 0.00013;  
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Qy 1 YGRKKRRQRRR 11  
Db 1 YGRKKRRQRRR 11

## RESULT 7

US-09-837-863-2  
; Sequence 2, Application US/09837863  
; Patent No. 6468754  
; GENERAL INFORMATION:  
; APPLICANT: Greene, Amy  
; APPLICANT: Zhou, Hua  
; APPLICANT: Thode, Silke  
; APPLICANT: Jarnigan, Kurt  
; TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption  
; TITLE OF INVENTION: of an Integrated DNA Sequence  
; FILE REFERENCE: 025.1US  
; CURRENT APPLICATION NUMBER: US/09/837,863  
; CURRENT FILING DATE: 2001-04-17  
; PRIOR APPLICATION NUMBER: US 60/198,498  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-837-863-2

Query Match 55.0%; Score 11; DB 2; Length 11;  
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11  
Db 1 YGRKKRRQRRR 11

## RESULT 8

US-09-660-742-1

; Sequence 1, Application US/09660742  
; Patent No. 6485977  
; GENERAL INFORMATION:  
; APPLICANT: Collmer, Alan  
; APPLICANT: Beer, Steven V.

; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND TECHNIQUES FOR DELIVERING TO  
; TITLE OF INVENTION: EUKARYOTIC CELLS BACTERIAL PROTEINS THAT ARE SECRETED  
; TITLE OF INVENTION: VIA TYPE III SECRETION SYSTEMS  
; FILE REFERENCE: 19603/4021

; CURRENT APPLICATION NUMBER: US/09/660,742  
; CURRENT FILING DATE: 2000-09-13

; PRIOR APPLICATION NUMBER: 60/153,507  
; PRIOR FILING DATE: 1999-09-13

; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1  
; LENGTH: 11

; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-660-742-1

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Db 1 YGRKKRRQRRR 11

## RESULT 9

US-09-434-345-2  
; Sequence 2, Application US/09434345  
; Patent No. 6511676  
; GENERAL INFORMATION:  
; APPLICANT: Boulikas, Tani  
; TITLE OF INVENTION: THERAPY FOR HUMAN CANCERS USING  
; TITLE OF INVENTION: CISPLATIN AND OTHER DRUGS OR GENES ENCAPSULATED INTO  
; TITLE OF INVENTION: LIPOSOMES  
; FILE REFERENCE: TB 2001.00  
; CURRENT APPLICATION NUMBER: US/09/434,345  
; CURRENT FILING DATE: 1999-11-05  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency Virus  
US-09-434-345-2

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11  
Db 1 YGRKKRRQRRR 11

## RESULT 10

US-09-632-287A-22  
; Sequence 22, Application US/09632287A  
; Patent No. 6521422  
; GENERAL INFORMATION:  
; APPLICANT: Hsu, Hailing  
; APPLICANT: Wooden, Scott K  
; APPLICANT: Boyle, William J  
; TITLE OF INVENTION: Fhm. A No. 6521422el Member of the TNF Ligand Supergene Family  
; FILE REFERENCE: 01017/35550A  
; CURRENT APPLICATION NUMBER: US/09/632,287A  
; CURRENT FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/147,294  
; PRIOR FILING DATE: 1999-08-04

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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide from the HIV TAT protein
US-09-632-287A-22

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Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 YGRKKRRQRRR 11

RESULT 11
US-09-632-277A-4
; Sequence 4, Application US/09632277A
; Patent No. 6599716
; GENERAL INFORMATION:
; APPLICANT: Heu, Hailing
; TITLE OF INVENTION: NTR3 A No. 6599716el Member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35549A
; CURRENT APPLICATION NUMBER: US/09/632,277A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,297
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV TAT peptide
US-09-632-277A-4

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Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YGRKKRRQRRR 11
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DB      1 YGRKKRRQRRR 11

RESULT 12
US-09-612-033B-15
; Sequence 15, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Satis, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmat2, a No. 6627199el Member of the TNF-Receptor Superfamily
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-612-033B-15
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Query Match      55.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 YGRKKRRQRRR 11

RESULT 13
US-09-780-070-37
; Sequence 37, Application US/09780070
; Patent No. 6632616
; GENERAL INFORMATION:
; APPLICANT: Burke, James
; APPLICANT: Strittmater, Warren
; APPLICANT: Nagai, Yoshitaka
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 5405.242
; CURRENT APPLICATION NUMBER: US/09/780,070
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/189,781
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-780-070-37

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DB      1 YGRKKRRQRRR 11

RESULT 14
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; Sequence 2, Application US/09775052A
; Patent No. 6645501
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48861/1742
; CURRENT APPLICATION NUMBER: US/09/775,052A
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-775-052A-2

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DB      1 YGRKKRRQRRR 11
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RESULT 15  
US-09-911-842A-6  
; Sequence 6, Application US/09911842A  
; Patent No. 6656707  
; GENERAL INFORMATION:  
; APPLICANT: Amgen Inc.  
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF  
; FILE REFERENCE: 01017/37592  
; CURRENT APPLICATION NUMBER: US/09/911,842A  
; CURRENT FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: US 60/222,438  
; PRIOR FILING DATE: 2000-08-01  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-911-842A-6  
  
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Db 1 YGRKKRRQRR 11

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Job time : 52 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2006, 23:52:28 ; Search time 182 Seconds  
(without alignments)  
50.903 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKKRRQRRRKPSADGHR 20

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

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Word size : 1

Total number of hits satisfying chosen parameters: 2090923

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	5	US-10-814-109-2
2	12	60.0	12	4	US-10-756-774-14
3	12	60.0	12	4	US-10-756-774-15
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13	11	55.0	11	3	US-09-780-070-37
14	11	55.0	11	3	US-09-815-108-9
15	11	55.0	11	3	US-09-886-404-13
16	11	55.0	11	3	US-09-805-805-8
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18	11	55.0	11	3	US-09-895-943-13
19	11	55.0	11	3	US-09-825-414-91
20	11	55.0	11	3	US-09-867-274-23
21	11	55.0	11	3	US-09-955-866-24
22	11	55.0	11	3	US-09-928-175-25
23	11	55.0	11	3	US-09-995-542-13
24	11	55.0	11	3	US-09-927-850-18
25	11	55.0	11	3	US-09-984-183-4
26	11	55.0	11	3	US-09-949-196-15
27	11	55.0	11	3	US-09-948-018-22

28	11	55.0	11	3	US-09-995-515-14	Sequence 14, Appl
29	11	55.0	11	3	US-09-895-593-13	Sequence 13, Appl
30	11	55.0	11	3	US-09-896-738-20	Sequence 20, Appl
31	11	55.0	11	3	US-09-981-286A-2	Sequence 2, Appl
32	11	55.0	11	3	US-09-134-793-2	Sequence 2, Appl
33	11	55.0	11	3	US-09-882-231-43	Sequence 43, Appl
34	11	55.0	11	3	US-09-775-052-2	Sequence 2, Appl
35	11	55.0	11	3	US-09-847-946A-124	Sequence 124, App
36	11	55.0	11	3	US-09-847-946A-125	Sequence 125, App
37	11	55.0	11	3	US-09-876-904A-5	Sequence 5, Appl
38	11	55.0	11	3	US-09-876-904A-10	Sequence 10, Appl
39	11	55.0	11	3	US-09-845-612B-20	Sequence 20, Appl
40	11	55.0	11	3	US-09-997-465B-2	Sequence 2, Appl
41	11	55.0	11	3	US-09-911-261A-18	Sequence 18, Appl
42	11	55.0	11	3	US-09-798-053-10	Sequence 10, Appl
43	11	55.0	11	3	US-09-779-791A-1	Sequence 1, Appl
44	11	55.0	11	3	US-09-810-927B-18	Sequence 18, Appl
45	11	55.0	11	4	US-10-007-363-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-10-814-109-2  
; Sequence 2, Application US/10814109  
; Publication No. US20050222042A1  
; GENERAL INFORMATION:  
; APPLICANT: Salter, Michael  
; APPLICANT: Gingrich, Jeffrey  
; TITLE OF INVENTION: Method for Modification of NMDA Receptors Through Inhibition of ;  
; FILE REFERENCE: 2560.004  
; CURRENT APPLICATION NUMBER: US/10/814,109  
; CURRENT FILING DATE: 2004-03-30  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-814-109-2

Query Match 100.0%; Score 20; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRKPSADGHR 20  
Db 1 YGRKKRRQRRRKPSADGHR 20

RESULT 2

US-10-756-774-14  
; Sequence 14, Application US/10756774  
; Publication No. US20040156859A1  
; GENERAL INFORMATION:  
; APPLICANT: Ezrin, Alan M.  
; APPLICANT: Fleiser, Angelica  
; APPLICANT: Robitaille, Martin  
; APPLICANT: Milner, Peter G.  
; APPLICANT: Bridon, Dominique P.  
; TITLE OF INVENTION: PULMONARY DELIVERY FOR BIOCONJUGATION  
; FILE REFERENCE: 500862001810  
; CURRENT APPLICATION NUMBER: US/10/756,774  
; CURRENT FILING DATE: 2004-01-12  
; PRIOR APPLICATION NUMBER: US 09/656,121  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: US 60/152,681  
; PRIOR FILING DATE: 1999-09-07  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 12

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-756-774-14

Query Match      60.0%; Score 12; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YGRKKRQRRRK 12

RESULT 3
US-10-756-774-15
; Sequence 15, Application US/10756774
; Publication No. US20040156859A1
; GENERAL INFORMATION:
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Fleiser, Angelica
; APPLICANT: Robitaille, Martin
; APPLICANT: Milner, Peter G.
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: PULMONARY DELIVERY FOR BIOCONJUGATION
; FILE REFERENCE: 500862001810
; CURRENT APPLICATION NUMBER: US/10/756,774
; CURRENT FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: US 09/656,121
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/152,681
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-756-774-15

Query Match      60.0%; Score 12; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRRK 12
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DB 1 YGRKKRQRRRK 12

RESULT 4
US-10-930-192-4
; Sequence 4, Application US/10930192
; Publication No. US20050059597A1
; GENERAL INFORMATION:
; APPLICANT: Tymianski, Michael
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
; FILE REFERENCE: 4438 0007
; CURRENT APPLICATION NUMBER: US/10/930,192
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: US 10/208,374
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/584,555
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-930-192-4

Query Match      60.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00015;
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QY 1 YGRKKRQRRRK 12
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DB 1 YGRKKRQRRRK 12

RESULT 5
US-10-930-192-5
; Sequence 5, Application US/10930192
; Publication No. US20050059597A1
; GENERAL INFORMATION:
; APPLICANT: Tymianski, Michael
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
; FILE REFERENCE: 4438 0007
; CURRENT APPLICATION NUMBER: US/10/930,192
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: US 10/208,374
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/584,555
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-930-192-5

Query Match      60.0%; Score 12; DB 5; Length 20;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRRK 12
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DB 1 YGRKKRQRRRK 12

RESULT 6
US-10-930-192-12
; Sequence 12, Application US/10930192
; Publication No. US20050059597A1
; GENERAL INFORMATION:
; APPLICANT: Tymianski, Michael
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
; FILE REFERENCE: 4438 0007
; CURRENT APPLICATION NUMBER: US/10/930,192
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: US 10/208,374
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/584,555
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-930-192-12

Query Match      60.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 YGRKKRQRRRK 12

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Qy 1 YGRKKRRQRRK 12  
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RESULT 7

US-11-021-928A-276  
; Sequence 276, Application US/11021928A  
; Publication No. US20050164933A1  
; GENERAL INFORMATION:

; APPLICANT: Tymianski, Michael  
; APPLICANT: Garman, Jonathan David  
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells  
; FILE REFERENCE: 1889-00800  
; CURRENT APPLICATION NUMBER: US/11/021,928A  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 11/021,928  
; PRIOR FILING DATE: 2004-12-22  
; NUMBER OF SEQ ID NOS: 384  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 276  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-021-928A-276

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Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRK 12  
Db 1 YGRKKRRQRRK 12

RESULT 8

US-11-021-928A-363  
; Sequence 363, Application US/11021928A  
; Publication No. US20050164933A1  
; GENERAL INFORMATION:

; APPLICANT: Tymianski, Michael  
; APPLICANT: Garman, Jonathan David  
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells  
; FILE REFERENCE: 1889-00800  
; CURRENT APPLICATION NUMBER: US/11/021,928A  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 11/021,928  
; PRIOR FILING DATE: 2004-12-22  
; NUMBER OF SEQ ID NOS: 384  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 363  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-021-928A-363

Query Match 60.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRK 12  
Db 1 YGRKKRRQRRK 12

RESULT 9

US-11-021-928A-364  
; Sequence 364, Application US/11021928A  
; Publication No. US20050164933A1

; GENERAL INFORMATION:  
; APPLICANT: Tymianski, Michael  
; APPLICANT: Garman, Jonathan David  
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells  
; FILE REFERENCE: 1889-00800  
; CURRENT APPLICATION NUMBER: US/11/021,928A  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 11/021,928  
; PRIOR FILING DATE: 2004-12-22  
; NUMBER OF SEQ ID NOS: 384  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 364  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-021-928A-364

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Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRK 12  
Db 1 YGRKKRRQRRK 12

RESULT 10

US-09-949-196-22  
; Sequence 22, Application US/09949196  
; Patent No. US20020147145A1  
; GENERAL INFORMATION:

; APPLICANT: Zealand Pharmaceuticals A/S  
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF Cdc25A IN RE  
; TITLE OF INVENTION: TO DNA DAMAGE  
; FILE REFERENCE: 55888 (45487)  
; CURRENT APPLICATION NUMBER: US/09/949,196  
; CURRENT FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence  
; NAME/KEY: BINDING  
; LOCATION: (22)..(22)  
; OTHER INFORMATION: NH2  
US-09-949-196-22

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RESULT 11

US-09-949-196-34  
; Sequence 34, Application US/09949196  
; Patent No. US20020147145A1  
; GENERAL INFORMATION:

; APPLICANT: Zealand Pharmaceuticals A/S  
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF Cdc25A IN RE  
; TITLE OF INVENTION: TO DNA DAMAGE  
; FILE REFERENCE: 55888 (45487)  
; CURRENT APPLICATION NUMBER: US/09/949,196  
; CURRENT FILING DATE: 2001-07-09

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; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
; NAME/KEY: BINDING
; LOCATION: (22)..(22)
; OTHER INFORMATION: NH2
US-09-949-198-34

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Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YGRKKRRQRRK 12

RESULT 12
US-09-779-791A-1
; Sequence 1, Application US/09779791A
; Publication No. US2001004417A1
; GENERAL INFORMATION:
; APPLICANT: Mirus Corporation
; APPLICANT: Wolff, Jon A
; APPLICANT: Monahan, Sean D
; APPLICANT: Budker, Vladimir G
; APPLICANT: Slatum, Paul M
; APPLICANT: Rozena, David B
; TITLE OF INVENTION: A Compound Containing a Labile Disulfide Bond
; FILE REFERENCE: Mirus 006.03
; CURRENT APPLICATION NUMBER: US/09/779,791A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 09/312,351
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-779-791A-1

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Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRR 11
Db 1 YGRKKRRQRRR 11

RESULT 13
US-09-780-070-37
; Sequence 37, Application US/09780070
; Patent No. US20020009752A1
; GENERAL INFORMATION:
; APPLICANT: Burke, James
; APPLICANT: Strittmatter, Warren
; APPLICANT: Nagai, Yoshitaka
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 5405.242
; CURRENT APPLICATION NUMBER: US/09/780,070
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/189,781
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-780-070-37

Query Match          55.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YGRKKRRQRRR 11

RESULT 14
US-09-815-108-9
; Sequence 9, Application US/09815108
; Patent No. US20020009776A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/815,108
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-815-108-9

Query Match          55.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YGRKKRRQRRR 11

RESULT 15
US-09-886-404-13
; Sequence 13, Application US/09886404
; Patent No. US2002037524A1
; GENERAL INFORMATION:
; APPLICANT: Medlock, Eugene
; APPLICANT: Yeh, Richard
; APPLICANT: Silbiger, Scott M.
; APPLICANT: Elliot, Gary S.
; APPLICANT: Nguyen, Hung Q.
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/37128B
; CURRENT APPLICATION NUMBER: US/09/886,404
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/810,384
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/266,159
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,125
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide of HIV
; OTHER INFORMATION: TAT protein
US-09-886-404-13

Query Match      55.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 YGRKKRRQRRR 11

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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:53:23 ; Search time 32 Seconds  
(without alignments)  
42.764 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKKRRQRRKPASDGHR 20

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications AA\_New.\*

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- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	11	55.0	11	7	US-11-223-610-45
6	11	55.0	11	7	US-11-267-986-8
7	11	55.0	11	7	US-11-267-817-19
8	11	55.0	11	7	US-11-271-285-59
9	11	55.0	11	7	US-11-317-806-85
10	11	55.0	11	7	US-11-238-035-39
11	11	55.0	11	7	US-11-250-830-1
12	11	55.0	11	7	US-11-241-836-16
13	11	55.0	12	7	US-11-264-074-19
14	11	55.0	14	7	US-11-142-051-4
15	11	55.0	14	7	US-11-318-535-7
16	11	55.0	14	7	US-11-318-535-8
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18	11	55.0	15	7	US-11-238-035-40
19	11	55.0	15	7	US-11-250-830-19
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25	11	55.0	34	7	US-11-223-610-46

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27	11	55.0	36	7	US-11-251-643-24	Sequence 24, Appl
28	11	55.0	36	7	US-11-286-920-6	Sequence 6, Appl
29	11	55.0	229	6	US-10-533-841-54	Sequence 54, Appl
30	11	55.0	293	6	US-10-533-841-52	Sequence 52, Appl
31	11	55.0	715	6	US-10-533-841-60	Sequence 60, Appl
32	11	55.0	779	6	US-10-547-530-82	Sequence 82, Appl
33	11	55.0	872	6	US-10-547-530-142	Sequence 142, Appl
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39	11	55.0	1003	6	US-10-547-530-124	Sequence 124, Appl
40	11	55.0	1035	6	US-10-533-841-67	Sequence 67, Appl
41	11	55.0	1078	6	US-10-533-841-71	Sequence 71, Appl
42	11	55.0	1141	6	US-10-533-841-79	Sequence 79, Appl
43	11	55.0	1141	6	US-10-533-841-81	Sequence 81, Appl
44	11	55.0	1141	6	US-10-533-841-83	Sequence 83, Appl
45	11	55.0	1141	6	US-10-533-841-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1  
US-10-547-530-78  
; Sequence 78, Application US/10547530  
; Publication No. US20060148086A1  
; GENERAL INFORMATION:  
; APPLICANT: Regents of the University of California, The  
; APPLICANT: Leonard, Rome H.  
; APPLICANT: Valerie, Kickhoefer A.  
; APPLICANT: Suina, Raval-Fernandes  
; APPLICANT: Phoebe, Stewart L.  
; TITLE OF INVENTION: Vault and Vault-like Carrier Molecules  
; FILE REFERENCE: 14399-1EP  
; CURRENT APPLICATION NUMBER: US/10/547,530  
; PRIOR FILING DATE: 2005-08-31  
; PRIOR APPLICATION NUMBER: 60/453,800  
; PRIOR FILING DATE: 2003-03-10  
; PRIOR APPLICATION NUMBER: PCT/US04/07434  
; PRIOR FILING DATE: 2004-03-10  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 78  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-10-547-530-78

Query Match 55.0%; Score 11; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.6e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRR 11  
| | | | | | | | | |  
Db 1 YGRKKRRQRR 11

RESULT 2  
US-10-518-710-4  
; Sequence 4, Application US/10518710  
; Publication No. US20060177431A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomizawa, Kazuhito  
; APPLICANT: Matsui, Hideki  
; TITLE OF INVENTION: Inhibitor of constitutive active forming of carcineurin  
; FILE REFERENCE: JP-13650  
; CURRENT APPLICATION NUMBER: US/10/518,710  
; CURRENT FILING DATE: 2004-12-22  
; NUMBER OF SEQ ID NOS: 6  
; SEQ ID NO 4

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; LENGTH: 11
; TYPE: PRT
; ORGANISM: HIV virus
US-10-518-710-4

Query Match          55.0%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
Db 1 YGRKKRQRRR 11

RESULT 3
US-10-559-806A-1
; Sequence 1, Application US/10559806A
; Publication No. US20060182736A1
; GENERAL INFORMATION:
; APPLICANT: KIM, JIN-SOO
; APPLICANT: SHIN, HYUN-CHUL
; APPLICANT: KWON, HEUNG-SUN
; TITLE OF INVENTION: TRANSDUCIBLE DNA-BINDING PROTEINS
; FILE REFERENCE: Q91925
; CURRENT APPLICATION NUMBER: US/10/559,806A
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: PCT/KR04/01385
; PRIOR FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: 60/477,459
; PRIOR FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-559-806A-1

Query Match          55.0%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
Db 1 YGRKKRQRRR 11

RESULT 4
US-11-318-535-24
; Sequence 24, Application US/11318535
; Publication No. US20060106197A1
; GENERAL INFORMATION:
; APPLICANT: Karas, Michael
; TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
; FILE REFERENCE: 002877.00028
; CURRENT APPLICATION NUMBER: US/11/318,535
; CURRENT FILING DATE: 2005-12-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-318-535-24

Query Match          55.0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
Db 1 YGRKKRQRRR 11

us-10-814-109-2.oligo.rapbn

RESULT 5
US-11-223-610-45
; Sequence 45, Application US/11223610
; Publication No. US20060111289A1
; GENERAL INFORMATION:
; APPLICANT: Mizejewski, Gerald J.
; TITLE OF INVENTION: Compositions and Methods of Using Alpha-Petoprotein Growth
; FILE REFERENCE: HOLLAND-09516
; CURRENT APPLICATION NUMBER: US/11/223,610
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-223-610-45

Query Match          55.0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
Db 1 YGRKKRQRRR 11

RESULT 6
US-11-267-986-8
; Sequence 8, Application US/11267986
; Publication No. US20060121505A1
; GENERAL INFORMATION:
; APPLICANT: Colamonic, Oscar
; APPLICANT: Siddiqui, Shahid
; TITLE OF INVENTION: Beta Chain-Associated Regulator of Apoptosis
; FILE REFERENCE: 02-135-D
; CURRENT APPLICATION NUMBER: US/11/267,986
; CURRENT FILING DATE: 2005-11-07
; PRIOR APPLICATION NUMBER: US 60/359,144
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: US 10/373,288
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/625,745
; PRIOR FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 11 amino acid protein internalization sequence signal based on t
US-11-267-986-8

Query Match          55.0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
Db 1 YGRKKRQRRR 11

RESULT 7
US-11-267-817-19
; Sequence 19, Application US/11267817
; Publication No. US20060148060A1
; GENERAL INFORMATION:
; APPLICANT: LEE, SANG-KYOU
```

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; APPLICANT: LEE, SEUNG-KYUO
; TITLE OF INVENTION: BIOMOLECULE TRANSDUCTION MOTIF MPH-1-BTM AND THE USE THEREOF
; FILE REFERENCE: 2435.0010002
; CURRENT APPLICATION NUMBER: US/11/267,817
; CURRENT FILING DATE: 2005-11-07
; PRIOR APPLICATION NUMBER: 10/501,665
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: KR 10-2002-0003183
; PRIOR FILING DATE: 2002-01-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: protein transduction domain
US-11-267-817-19

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Query Match          55.0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 YGRKKRQRRR 11
   |||||
Db 1 YGRKKRQRRR 11

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RESULT 8
US-11-271-285-59
; Sequence 59, Application US/11271285
; Publication No. US20060148700A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Tanaka, Masashi
; APPLICANT: Robbins, Robert C.
; TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplanted
; FILE REFERENCE: 58600-8218.US00
; CURRENT APPLICATION NUMBER: US/11/271,285
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US 60/626,564
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus 1
US-11-271-285-59

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Query Match          55.0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 YGRKKRQRRR 11
   |||||
Db 1 YGRKKRQRRR 11

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RESULT 9
US-11-317-806-85
; Sequence 85, Application US/11317806
; Publication No. US20060148702A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Bright, Rachel
; TITLE OF INVENTION: Methods of Increasing Cerebral Blood Flow
; FILE REFERENCE: 58600-8214.US00
; CURRENT APPLICATION NUMBER: US/11/317,806
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: US 60/641,413
; PRIOR FILING DATE: 2005-01-04

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; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus 1
US-11-317-806-85

Query Match          55.0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
   |||||
Db 1 YGRKKRQRRR 11

RESULT 10
US-11-238-035-39
; Sequence 39, Application US/11238035
; Publication No. US20060160181A1
; GENERAL INFORMATION:
; APPLICANT: Luethy, Roland
; APPLICANT: Yang, Robert
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Sarosi, Iidiko
; TITLE OF INVENTION: Fibroblast Growth Factor-23 Molecules and Uses Thereof
; FILE REFERENCE: 01-004
; CURRENT APPLICATION NUMBER: US/11/238,035
; CURRENT FILING DATE: 2005-09-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-238-035-39

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Query Match          55.0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 YGRKKRQRRR 11
   |||||
Db 1 YGRKKRQRRR 11

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RESULT 11
US-11-250-830-1
; Sequence 1, Application US/11250830
; Publication No. US20060159619A1
; GENERAL INFORMATION:
; APPLICANT: BECKER, MATTHEW L.
; APPLICANT: FANG, HUAPENG
; APPLICANT: LI, XIAOXU
; APPLICANT: PAN, DIPANJAN
; APPLICANT: ROSSIN, RAFFAELLA
; APPLICANT: SUN, XIANKAI
; APPLICANT: TAYLOR, JOHN-STEPHEN
; APPLICANT: TURNER, JEFFREY L.
; APPLICANT: WELCH, MICHAEL JOHN
; APPLICANT: WOOLEY, KAREN L.
; TITLE OF INVENTION: CELL PERMEABLE NANOCONJUGATES OF SHELL-CROSSLINKED
; TITLE OF INVENTION: KNEDEL (SCK) AND PEPTIDE NUCLEIC ACIDS ("PNAs") WITH
; TITLE OF INVENTION: UNIQUELY EXPRESSED OR OVER-EXPRESSED mRNA TARGETING
; TITLE OF INVENTION: SEQUENCES FOR EARLY DIAGNOSIS AND THERAPY OF CANCER
; FILE REFERENCE: 15060-75
; CURRENT APPLICATION NUMBER: US/11/250,830
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,242
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 3.3

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Fri Aug 25 11:24:29 2006

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; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-250-830-1

Query Match          55.0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
DB 1 YGRKKRQRRR 11

RESULT 12
US-11-241-836-16
; Sequence 16, Application US/11241836
; Publication No. US20060168672A1
; GENERAL INFORMATION:
; APPLICANT: Welch, Andrew
; APPLICANT: Sarmiento, Ulla
; APPLICANT: Schultz, Henry
; APPLICANT: Chute, Hilary
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
; FILE REFERENCE: 01-668-G
; CURRENT APPLICATION NUMBER: US/11/241,836
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: 60/214,512
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 09/729,264
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-241-836-16

Query Match          55.0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
DB 1 YGRKKRQRRR 11

RESULT 13
US-11-264-074-19
; Sequence 19, Application US/11264074
; Publication No. US20060148104A1
; GENERAL INFORMATION:
; APPLICANT: Marini, et al
; TITLE OF INVENTION: Detection and Ion Channel or Receptor Activity
; FILE REFERENCE: 0492611-0647
; CURRENT APPLICATION NUMBER: US/11/264,074
; CURRENT FILING DATE: 2005-10-31
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: TAT peptide
US-11-264-074-19

Query Match          55.0%; Score 11; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-250-830-1

Query Match          55.0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
DB 1 YGRKKRQRRR 11

RESULT 14
US-11-142-051-4
; Sequence 4, Application US/11142051
; Publication No. US20060105956A1
; GENERAL INFORMATION:
; APPLICANT: Pincus, Matthew
; APPLICANT: Michl, Josef
; TITLE OF INVENTION: PHENOTYPIC REVERSION OF PANCREATIC CARCINOMA CELLS
; FILE REFERENCE: 1181-26
; CURRENT APPLICATION NUMBER: US/11/142,051
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US 60/575,131
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/575,846
; PRIOR FILING DATE: 2004-05-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide; HIV-1 TAT membrane penetrating sequence
US-11-142-051-4

Query Match          55.0%; Score 11; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
DB 1 YGRKKRQRRR 11

RESULT 15
US-11-318-535-7
; Sequence 7, Application US/11318535
; Publication No. US20060106197A1
; GENERAL INFORMATION:
; APPLICANT: Karas, Michael
; TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
; FILE REFERENCE: 002877.00028
; CURRENT APPLICATION NUMBER: US/11/318,535
; CURRENT FILING DATE: 2005-12-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: protein transduction domain
; NAME/KEY: MISC.FEATURE
; LOCATION: (1)-(1)
; OTHER INFORMATION: Biotin
US-11-318-535-7

Query Match          55.0%; Score 11; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
DB 4 YGRKKRQRRR 14

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Search completed: August 24, 2006, 23:56:54  
Job time : 32 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:46:43 ; Search time 38 Seconds  
(without alignments)  
50.640 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKKRRQRRRKPASADGHR 20

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	55.0	71	2 T09384	trans-activating t
2	11	55.0	72	1 TNLJH4	trans-activating t
3	11	55.0	86	1 TNLJZR	trans-activating t
4	11	55.0	86	2 A25700	trans-activating t
5	11	55.0	86	2 JC5591	transactivator pro
6	11	55.0	86	2 S54381	tat protein - huma
7	11	55.0	86	2 S33982	trans-activating t
8	11	55.0	87	2 T01665	tat protein - huma
9	11	55.0	95	1 TNLJ12	trans-activating t
10	11	55.0	101	1 E44001	trans-activating t
11	11	55.0	101	2 T09446	tat protein - huma
12	10	50.0	86	1 TNLJND	trans-activating t
13	9	45.0	541	1 A43610	protein-tyrosine k
14	9	45.0	542	1 TVHUSC	protein-tyrosine k
15	7	35.0	143	2 AF2781	hypothetical prote
16	7	35.0	668	2 T29884	hypothetical prote
17	7	35.0	1951	2 S00320	sodium channel pro
18	7	35.0	1983	2 A60054	sodium channel pro
19	6	30.0	29	2 S08555	ribosomal protein
20	6	30.0	46	2 AI0560	probable 50s ribos
21	6	30.0	53	4 S16048	probable pilin Ngr
22	6	30.0	78	2 E97064	hypothetical prote
23	6	30.0	80	2 T01320	NOI protein, nitra
24	6	30.0	80	2 C95994	hypothetical prote
25	6	30.0	81	2 T47865	transport protein
26	6	30.0	100	1 TNLJSI	trans-activating t
27	6	30.0	103	1 VKLJGG	trans-regulatory s
28	6	30.0	108	1 VKLJS2	trans-regulatory s
29	6	30.0	108	2 A13250	virA/G regulated p

30	6	30.0	109	2 S12338	virH protein - Agr
31	6	30.0	117	2 A75220	hypothetical prote
32	6	30.0	119	2 T49848	hypothetical prote
33	6	30.0	142	2 E96711	F24J5.7 [imported]
34	6	30.0	144	2 F70895	probable PE protei
35	6	30.0	148	2 T02352	hypothetical prote
36	6	30.0	153	2 B84324	S05 ribosomal prot
37	6	30.0	162	2 T12538	hypothetical prote
38	6	30.0	174	2 T46382	hypothetical prote
39	6	30.0	199	2 D90005	thymidine kinase (
40	6	30.0	216	2 F84201	hypothetical prote
41	6	30.0	218	2 G82786	conserved hypotet
42	6	30.0	234	2 S27956	arginine-rich prot
43	6	30.0	256	2 T25707	hypothetical prote
44	6	30.0	267	2 G83206	hypothetical prote
45	6	30.0	275	2 C81027	lacto-N-neotetraos

ALIGNMENTS

RESULT 1

T09384

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 31-Dec-2004

C:Accession: T09384

R:Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Bir

J. Virol. 69, 4228-4236, 1995

A:Title: Defective accessory genes in a human immunodeficiency virus type 1-infected lor

A:Reference number: Z16654; MUID:95287475; PMID:7769682

A:Accession: T09384

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-71 <MIC>

C:Cross-references: UNIPROT:O71926; UNIPARC:UPI00000FF00C; EMBL:U24451; NID:g829440; PII

C:Gene: tat

C:Superfamily: leukemia virus trans-activating transcription regulator

C:Keywords: transcription

Query Match 55.0%; Score 11; DB 2; Length 71;  
Best Local Similarity 100.0%; Pred. No. 0.00034;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YGRKKRRQRRR 11

Db 47 YGRKKRRQRRR 57

RESULT 2

TNLJH4

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 31-Dec-2004

C:Accession: B25523

R:Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,

Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986

A:Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human

A:Reference number: A94136; MUID:87041461; PMID:3490666

A:Accession: B25523

A:Molecule type: DNA

A:Residues: 1-72 <DES>

A:Cross-references: UNIPARC:UPI0000174A55; GB:M13137; NID:g326460

A:Note: the GenBank entry ADRE3AA FID:g209908 differs from the published sequence in tra

C:Gene: tat

C:Superfamily: leukemia virus trans-activating transcription regulator

C:Keywords: transcription regulation

Query Match 55.0%; Score 11; DB 1; Length 72;  
Best Local Similarity 100.0%; Pred. No. 0.00034;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





QY 1 YGRKKRRQRRR 11  
 |||||  
 Db 47 YGRKKRRQRRR 57

RESULT 8  
 T01665  
 tat protein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C>Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 31-Dec-2004  
 C:Accession: T01665  
 R:Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.  
 Cell 46, 63-74, 1986  
 A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates  
 A:Reference number: Z14389; MUID:86245056; PMID:2424612  
 A:Accession: T01665  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-87 <ALI>  
 A:Cross-references: UNIPROT:P04613; UNIPARC:UPI00001132A9; EMBL:K03456; NID:G60228; PIDN:G60228  
 C:Genetics:  
 A:Introns: 72/2  
 C:Superfamily: leukemia virus trans-activating transcription regulator

Query Match 55.0%; Score 11; DB 2; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 0.0004;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11  
 |||||  
 Db 47 YGRKKRRQRRR 57

RESULT 9  
 TNLJ12  
 trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C>Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 31-Dec-2004  
 C:Accession: A04017  
 R:Araya, S.K.; Gallo, R.C.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986  
 A:Title: Three novel genes of human T-lymphotropic virus type III: Immune reactivity of  
 A:Reference number: A94093; MUID:86177573; PMID:3008154  
 A:Accession: A04017  
 A:Molecule type: DNA  
 A:Residues: 1-95 <ARY>  
 A:Cross-references: UNIPROT:P04326; UNIPARC:UPI0000174A54  
 C:Genetics:  
 A:Gene: tat  
 C:Superfamily: leukemia virus trans-activating transcription regulator  
 C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 55.0%; Score 11; DB 1; Length 95;  
 Best Local Similarity 100.0%; Pred. No. 0.00043;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11  
 |||||  
 Db 56 YGRKKRRQRRR 66

RESULT 10  
 E44001  
 trans-activating transcription regulator - human immunodeficiency virus type 1 (strain X  
 N:Alternate names: tat protein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Dec-2004  
 C:Accession: E44001  
 R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.  
 J. Virol. 66, 6587-6600, 1992  
 A:Title: Complete nucleotide sequence, genome organization, and biological properties of

A:Reference number: A44001; MUID:93021387; PMID:1404605  
 A:Accession: E44001  
 A:Molecule type: DNA  
 A:Residues: 1-101 <LIY>  
 A:Cross-references: UNIPROT:P35965; UNIPARC:UPI0000136937; GB:M93258  
 C:Genetics:  
 A:Gene: tat  
 A:Introns: 72/2  
 C:Superfamily: leukemia virus trans-activating transcription regulator  
 C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 55.0%; Score 11; DB 1; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 0.00045;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11  
 |||||  
 Db 47 YGRKKRRQRRR 57

RESULT 11  
 T09446  
 tat protein - human immunodeficiency virus type 1 (strain JRF1)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 31-Dec-2004  
 C:Accession: T09446  
 R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,  
 submitted to the EMBL Data Library, July 1996  
 A:Reference number: Z16673  
 A:Accession: T09446  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-101 <PAN>  
 A:Cross-references: UNIPROT:Q75758; UNIPARC:UPI0000109776; EMBL:U63632; NID:G1465777; PI  
 C:Genetics:  
 A:Gene: tat  
 A:Introns: 72/2  
 C:Superfamily: leukemia virus trans-activating transcription regulator

Query Match 55.0%; Score 11; DB 2; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 0.00045;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11  
 |||||  
 Db 47 YGRKKRRQRRR 57

RESULT 12  
 TNLJND  
 trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 31-Dec-2004  
 C:Accession: JQ0071  
 R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;  
 Gene 81, 275-284, 1989  
 A:Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immun  
 A:Reference number: JQ0085; MUID:90034200; PMID:2806917  
 A:Accession: JQ0071  
 A:Molecule type: DNA  
 A:Residues: 1-86 <SPI>  
 A:Cross-references: UNIPROT:P18804; UNIPARC:UPI000011D5D6; GB:M27323; NID:G328154; PIDN:  
 C:Genetics:  
 A:Gene: tat  
 C:Superfamily: leukemia virus trans-activating transcription regulator  
 C:Keywords: AIDS; immunodeficiency; transcription

Query Match 50.0%; Score 10; DB 1; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 0.0038;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRR 10

Db

47 YGKRRQR 56

|||||

RESULT 13

A3610

protein-tyrosine kinase (EC 2.7.1.112) src, neuronal [similarity] - mouse

N:Alternate names: Rouse sarcoma oncogene

C:Species: Mus musculus (house mouse)

C>Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 05-Oct-2004

A:Accession: A3610

R:Martiniz, R.; Mathey-Prevot, B.; Bernards, A.; Baltimore, D.

Science 237, 411-415, 1987

A>Title: Neuronal pp60(c-src) contains a six-amino acid insertion relative to its non-neuronal counterpart

A:Reference number: A43610; MUID:87263406; PMID:2440106

A:Accession: A43610

A:Molecule type: mRNA

A:Residues: 1-541 <NAR>

A:CROSS-references: UNIPROT:P05480; UNIPARC:UPI0000161D19; GB:M17031; NID:G201056; PIDN:G201056

C:Comment: The neuronal c-src has an 6 residue insertion of RLNVNR within the amino-terminal region

C:Genetics:

A:Gene: Src

A:CROSS-references: MGI:98397

A:Map position: 2:91.0

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phosphatase

F:90-145/Domain: SH3 homology <SH3>

F:156-253/Domain: SH2 homology <SH2>

F:273-531/Domain: protein kinase homology <KIN>

F:281-289/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:303/Active site: Lys #status predicted

F:424,535/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match

Best Local Similarity

Matches

45.0%;

Score 9;

DB 1;

Length 541;

100.0%;

Pred. No. 0.15;

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

12 KPASADGHR 20

|||||

Db

39 KPASADGHR 47

|||||

RESULT 14

TVHUSC

protein-tyrosine kinase (EC 2.7.1.112) src, neuronal - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1989 #sequence\_revision 07-Oct-1994 #text\_change 05-Oct-2004

C:Accession: A26891; A61083; A23287; A28832; B34704

R:Tanaka, A.; Gibbs, C.P.; Arthur, R.R.; Anderson, S.K.; Kung, H.J.; Fujita, D.J.

Mol. Cell. Biol. 7, 1978-1983, 1987

A>Title: DNA sequence encoding the amino-terminal region of the human c-src protein: implications for the structure and function of the protein

A:Reference number: A26891; MUID:87257903; PMID:3299057

A:Accession: A26891

A:Molecule type: mRNA

A:Residues: 1-117;124-191 <TAN>

A:CROSS-references: UNIPROT:P12931; UNIPARC:UPI0000172578; UNIPARC:UPI0000172579; GB:M1610

R:Pyper, J.M.; Bolen, J.B.

J. Neurosci. Res. 24, 89-96, 1989

A>Title: Neuron-specific splicing of C-SRC RNA in human brain.

A:Reference number: A61083; MUID:90040822; PMID:2681803

A:Accession: A61083

A:Molecule type: mRNA

A:Residues: 98-145 <PYP>

A:CROSS-references: UNIPARC:UPI000017257A

A:Accession: B61083

A:Molecule type: mRNA

A:Residues: 98-117;124-145 <PY2>

A:CROSS-references: UNIPARC:UPI000017257A

R:Anderson, S.K.; Gibbs, C.P.; Tanaka, A.; Kung, H.J.; Fujita, D.J.

Mol. Cell. Biol. 5, 1122-1129, 1985

A>Title: Human cellular src gene: Nucleotide sequence and derived amino acid sequence of the src gene

A:Reference number: A23287; MUID:85213483; PMID:2582238

Query Match

Best Local Similarity

Matches

45.0%;

Score 9;

DB 1;

Length 541;

100.0%;

Pred. No. 0.15;

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

12 KPASADGHR 20

|||||

Db

39 KPASADGHR 47

|||||

A:Accession: A23287

A:Molecule type: mRNA

A:Residues: 192-542 <AND>

A:CROSS-references: UNIPARC:UPI000016B068; GB:X02647; NID:G36588; PIDN:CAA26485.1; PID:G36588

R:Parker, R.C.; Mardon, G.; Lebo, R.V.; Varmus, H.E.; Bishop, J.W.

Mol. Cell. Biol. 5, 831-838, 1985

A>Title: Isolation of duplicated human c-src genes located on chromosomes 1 and 20.

A:Reference number: A28832; MUID:85187981; PMID:2581127

A:Accession: A28832

A:Molecule type: mRNA

A:Residues: 382-542 <PAR>

A:CROSS-references: UNIPARC:UPI000017257D

R:Pyper, J.M.; Bolen, J.B.

Mol. Cell. Biol. 10, 2035-2040, 1990

A>Title: Identification of a novel neuronal C-SRC exon expressed in human brain.

A:Reference number: A34704; MUID:90220588; PMID:1691439

A:Accession: B34704

A:Molecule type: mRNA

A:Residues: 118-123 <PY3>

A:CROSS-references: UNIPARC:UPI000017257E

C:Genetics:

A:Gene: GDB:SRC

A:CROSS-references: GDB:120750; OMIM:190090

A:Map position: 20q11.2-20q11.2

A:Introns: 84/1; 117/2; 123/2; 156/2; 191/1; 241/1; 293/1; 353/1; 378/3; 430/1; 474/1

C:Function:

A>Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phosphatase

F:1-542/Product: protein-tyrosine kinase src, neuronal #status predicted <NAR>

F:1-117,124-542/Product: protein-tyrosine kinase src, short form #status predicted <MA2>

F:91-146/Domain: SH3 homology <SH3>

F:157-254/Domain: SH2 homology <SH2>

F:274-532/Domain: protein kinase homology <KIN>

F:282-290/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:304/Active site: Lys #status predicted

F:425,536/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match

Best Local Similarity

Matches

45.0%;

Score 9;

DB 1;

Length 542;

100.0%;

Pred. No. 0.15;

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

12 KPASADGHR 20

|||||

Db

40 KPASADGHR 48

|||||

RESULT 15

AF2781

hypothetical protein Atul668 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004

C:Accession: AF2781

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.

A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AF2781

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-143 <KUR>

A:CROSS-references: UNIPROT:O8UET7; UNIPARC:UPI00000D1C2E; GB:AE009686; PIDN:AAI42668.1

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atul668

A:Map position: circular chromosome

Query Match

Best Local Similarity

Matches

35.0%;

Score 7;

DB 2;

Length 143;

Best Local Similarity 100.0%; Pred. No. 5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KRRQRR 11  
| | | | |  
Db 41 KRRQRR 47

Search completed: August 24, 2006, 23:52:12  
Job time : 40 secs

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GenCore version 5.1.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2006, 23:43:13 ; Search time 300 Seconds  
(without alignments)  
61.668 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKKRRQRRKPASADGHR 20

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 92501592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849579

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Uniprot\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	60.0	86	Q6Y0V6_9HIV1	Q6Y0V6 human immun
2	11	55.0	58	TAT_HV1B5	P04612 human immun
3	11	55.0	64	Q6QAV2_9HIV1	Q6QAV2 human immun
4	11	55.0	65	Q75540_9HIV1	Q75540 human immun
5	11	55.0	65	Q75544_9HIV1	Q75544 human immun
6	11	55.0	68	Q6QAV4_9HIV1	Q6QAV4 human immun
7	11	55.0	70	Q66MQ1_9HIV1	Q66mq1 human immun
8	11	55.0	71	O40224_9HIV1	O40224 human immun
9	11	55.0	71	O40225_9HIV1	O40225 human immun
10	11	55.0	71	O40226_9HIV1	O40226 human immun
11	11	55.0	71	O40227_9HIV1	O40227 human immun
12	11	55.0	71	O40228_9HIV1	O40228 human immun
13	11	55.0	71	O40231_9HIV1	O40231 human immun
14	11	55.0	71	O40232_9HIV1	O40232 human immun
15	11	55.0	71	O40233_9HIV1	O40233 human immun
16	11	55.0	71	O40234_9HIV1	O40234 human immun
17	11	55.0	71	Q389T9_9HIV1	Q389t9 human immun
18	11	55.0	71	Q389U6_9HIV1	Q389u6 human immun
19	11	55.0	71	Q389W0_9HIV1	Q389w0 human immun
20	11	55.0	71	Q389W8_9HIV1	Q389w8 human immun
21	11	55.0	71	Q58PY1_9HIV1	Q58py1 human immun
22	11	55.0	71	Q58Q03_9HIV1	Q58q03 human immun
23	11	55.0	71	Q58Q10_9HIV1	Q58q10 human immun
24	11	55.0	71	Q58Q64_9HIV1	Q58q64 human immun
25	11	55.0	71	Q58Q69_9HIV1	Q58q69 human immun
26	11	55.0	71	Q58Q75_9HIV1	Q58q75 human immun
27	11	55.0	71	Q58Q43_9HIV1	Q58q43 human immun
28	11	55.0	71	Q58Q44_9HIV1	Q58q44 human immun
29	11	55.0	71	Q58Q45_9HIV1	Q58q45 human immun
30	11	55.0	71	Q58Q46_9HIV1	Q58q46 human immun
31	11	55.0	71	Q58Q47_9HIV1	Q58q47 human immun

32	11	55.0	71	2	Q5UG48_9HIV1	Q5ug48 human immun
33	11	55.0	71	2	Q5UG52_9HIV1	Q5ug52 human immun
34	11	55.0	71	2	Q5UG53_9HIV1	Q5ug53 human immun
35	11	55.0	71	2	Q5UG54_9HIV1	Q5ug54 human immun
36	11	55.0	71	2	Q5UG55_9HIV1	Q5ug55 human immun
37	11	55.0	71	2	Q5UG56_9HIV1	Q5ug56 human immun
38	11	55.0	71	2	Q5UG57_9HIV1	Q5ug57 human immun
39	11	55.0	71	2	Q5UG58_9HIV1	Q5ug58 human immun
40	11	55.0	71	2	Q5UG59_9HIV1	Q5ug59 human immun
41	11	55.0	71	2	Q5UG60_9HIV1	Q5ug60 human immun
42	11	55.0	71	2	Q5UG61_9HIV1	Q5ug61 human immun
43	11	55.0	71	2	Q5UG62_9HIV1	Q5ug62 human immun
44	11	55.0	71	2	Q5UG64_9HIV1	Q5ug64 human immun
45	11	55.0	71	2	Q5UG65_9HIV1	Q5ug65 human immun

ALIGNMENTS

RESULT 1  
Q6Y0V6\_9HIV1 PRELIMINARY; PRT; 86 AA.  
AC Q6Y0V6\_9HIV1 PRELIMINARY; PRT; 86 AA.  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE Tat protein (Fragment).  
GN Name=tat;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22912857; PubMed=14551888; DOI=10.1086/378412;  
RG The Tat Multicentric Study Group;  
RA Butto S., Fiorelli V., Tripiciano A., Ruiz-Alvarez M.J., Scoglio A.,  
RA Ensoli F., Ciccozzi M., Collacchi B., Sabbatucci M., Cafaro A.,  
RA Guzman C.A., Borsetti A., Caputo A., Vardas E., Colvin M., Lukwiya M.,  
RA Rezza G., Ensoli B.;  
RT "Sequence Conservation and Antibody Cross-Recognition of Clade B Human  
RT Immunodeficiency Virus (HIV) type 1 Tat Protein in HIV-1-Infected  
RL Italians, Ugandans, and South Africans."  
RL J. Infect. Dis. 188:1171-1180(2003).  
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CC -----  
DR EMBL; AY193998; AAP33727.1; -; Genomic\_DNA.  
DR HSSP; P04613; 1KSK.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR GO; GO:0006350; P:transcription; IEA.  
DR InterPro; IPR001831; IV\_Tat.  
DR Pfam; PF00539; Tat; 1.  
DR PRINTS; PR00055; HIVTATDOMAIN.  
DR Activator; Nuclear protein; RNA-binding; Transcription;  
KW Transcription regulation.  
FT NON\_TER 86  
SQ SEQUENCE 86 AA; 9840 MW; AD27037029ACA0EA CRC64;

Query Match 60.0%; Score 12; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred.No. 0.00011;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRK 12

Db 47 YGRKKRRQRRRK 58

```

RESULT 2
TAT HV1B5          STANDARD;          PRT;          58 AA.
AC P04612;
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT 13-AUG-1987, sequence version 1.
DT 07-FEB-2006, entry version 40.
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN Name=TAT;
OS Human immunodeficiency virus type 1 (isolate BH5) (HIV-1).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11682;
RN
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W.A., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafaleki J.A., Whitehorn E.A.,
RA Baumdister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).
CC -1- FUNCTION: Transcriptional regulator that acts by binding to the
CC trans-activating responsive sequence (TAR) RNA element and
CC activates transcription initiation and/or elongation from the LTR
CC promoter.
CC -1- SUBUNIT: Binds cyclin T1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; K02012; AAA44656.1; -; Genomic_RNA.
CC HSSP; P04610; 1JFW.
CC SMR; P04612; 1-47.
CC HIV; K02012; TAT$BH5.
CC InterPro; IPR001831; IV_Tat.
CC Pfam; PF00539; Tat; 1.
CC PRINTS; PR00055; HIVTATDOMAIN.
CC Activator; AIDS; Nuclear protein; RNA-binding; Transcription;
CC Transcription regulation.
CC CHAIN 1 >58 TAT protein.
CC NON_TER 58 58 /FTID=PRO_0000085343.
CC SEQUENCE 58 AA; 6800 MW; E36C21F8FD813E3 CRC64;

Query Match 55.0%; Score 11; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKRRQRRR 11
Db 47 YGRKRRQRRR 57

RESULT 3
Q6QAV2_9HIV1
ID Q6QAV2_9HIV1 PRELIMINARY; PRT; 64 AA.
AC Q6QAV2;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15157352; DOI=10.1089/08892204323048087;
RA Andreo S.M.S., Barra L.A.C., Costa L.J., Sucupira M.C.A.,

Query Match 55.0%; Score 11; DB 1; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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RA Souza I.E.L., Diaz R.S.;
RT "HIV Type 1 Transmission by Human Bite.";
RL AIDS Res. Hum. Retroviruses 20:349-350(2004).
CC
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CC
CC EMBL; AY549944; AAS67918.1; -; Genomic_DNA.
CC SMR; Q6QAV2; 1-64.
CC DR GO; GO:0042025; C:host cell nucleus; IEA.
CC DR GO; GO:0005634; C:nucleus; IEA.
CC DR GO; GO:0003723; F:RNA binding; IEA.
CC DR GO; GO:0003700; F:transcription factor activity; IEA.
CC DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC DR GO; GO:0006350; P:transcription; IEA.
CC DR InterPro; IPR001831; IV_Tat.
CC DR Pfam; PF00539; Tat; 1.
CC DR PRINTS; PR00055; HIVTATDOMAIN.
CC DR Activator; Nuclear protein; RNA-binding; Transcription;
CC Transcription regulation.
CC KW NON_TER 1
CC FT NON_TER 1
CC SQ SEQUENCE 64 AA; 7474 MW; E13926D6C42D72D3 CRC64;

Query Match 55.0%; Score 11; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKRRQRRR 11
Db 39 YGRKRRQRRR 49

RESULT 4
Q75540_9HIV1
ID Q75540_9HIV1 PRELIMINARY; PRT; 65 AA.
AC Q75540;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; U57248; AAB17808.1; -; Genomic_DNA.
CC DR HSSP; P12506; 1TBC.
CC DR GO; GO:0042025; C:host cell nucleus; IEA.
CC DR GO; GO:0005634; C:nucleus; IEA.
CC DR GO; GO:0003723; F:RNA binding; IEA.
CC DR GO; GO:0003700; F:transcription factor activity; IEA.
CC DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC DR GO; GO:0006350; P:transcription; IEA.
CC DR InterPro; IPR001831; IV_Tat.
CC DR Pfam; PF00539; Tat; 1.
CC DR PRINTS; PR00055; HIVTATDOMAIN.
CC DR Activator; Nuclear protein; RNA-binding; Transcription;
CC Transcription regulation.
CC KW NON_TER 1
CC FT NON_TER 1
CC SQ SEQUENCE 65 AA; 7619 MW; 91584F861A2F9736 CRC64;

Query Match 55.0%; Score 11; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YGRKKRQRRR 11
DB 47 YGRKKRQRRR 57

RESULT 5
Q75544_9HIV1
ID Q75544_9HIV1 PRELIMINARY; PRT; 65 AA.
AC Q75544;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; U57252; AAB17812.1; -; Genomic_DNA.
DR HSP; P12506; 1TBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 1
SQ SEQUENCE 65 AA; 7677 MW; 91584F861F6A8362 CRC64;

Query Match 55.0%; Score 11; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
DB 47 YGRKKRQRRR 57

RESULT 6
Q6QAV4_9HIV1
ID Q6QAV4_9HIV1 PRELIMINARY; PRT; 68 AA.
AC Q6QAV4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Andreo S.M.S., Barra L.A.C., Costa L.J., Sucupira M.C.A.,
RA Souza I.E.L., Diaz R.S.;
RT "HIV Type 1 Transmission by Human Bite.";
RL AIDS Res. Hum. Retroviruses 20:349-350(2004).
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CC
DR EMBL; AY549942; AAS67916.1; -; Genomic_DNA.
DR SMR; O6QAV4; 1-68.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 1
SQ SEQUENCE 68 AA; 7983 MW; 326A05D50078CD29 CRC64;

Query Match 55.0%; Score 11; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 0.00095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
DB 43 YGRKKRQRRR 53

RESULT 7
Q66MQ1_9HIV1
ID Q66MQ1_9HIV1 PRELIMINARY; PRT; 70 AA.
AC Q66MQ1;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Herring B.L., Grant R.M., Delwart E.L.;
RT "No superinfection among seroconcordant couples after well-defined
RT exposure.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AY686119; AAU05440.1; -; Genomic_RNA.
DR SMR; O66MQ1; 1-70.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 70
SQ SEQUENCE 70 AA; 8096 MW; 28E39B5672863DBB CRC64;

Query Match 55.0%; Score 11; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.00098;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
DB 47 YGRKKRQRRR 57
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```

RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
and tat1 genes derived from individuals with different rates of
disease progression.";
RL Virology 232:319-331(1997).
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CC EMBL; AF000523; AAB62522.1; -; Genomic_DNA.
DR HSSP; P12506; 1TBC.
DR SMR; O40225; 1-66.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA. IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 71
SQ SEQUENCE 71 AA; 8179 MW; CE411588EB96209F CRC64;

Query Match 55.0%; Score 11; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11
DB 47 YGRKKRRQRRR 57

RESULT 8
O40224_9HIV1 PRELIMINARY; PRT; 71 AA.
AC O40224_
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=AD93-A3tat;
RC MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RX Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
and tat1 genes derived from individuals with different rates of
disease progression.";
RL Virology 232:319-331(1997).
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-----
CC EMBL; AF000522; AAB62521.1; -; Genomic_DNA.
DR HSSP; P04610; 1JFW.
DR SMR; O40224; 1-71.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 71
SQ SEQUENCE 71 AA; 8211 MW; B3031C7AF5EF30E0 CRC64;

Query Match 55.0%; Score 11; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11
DB 47 YGRKKRRQRRR 57

RESULT 9
O40225_9HIV1 PRELIMINARY; PRT; 71 AA.
AC O40225_
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=BJ93-A3tat;
RC MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RX Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
and tat1 genes derived from individuals with different rates of
disease progression.";
RL Virology 232:319-331(1997).
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CC EMBL; AF000524; AAB62523.1; -; Genomic_DNA.
DR HSSP; P04610; 1JFW.
DR SMR; O40226; 1-71.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.

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RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
and tat1 genes derived from individuals with different rates of
disease progression.";
RL Virology 232:319-331(1997).
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CC EMBL; AF000523; AAB62522.1; -; Genomic_DNA.
DR HSSP; P12506; 1TBC.
DR SMR; O40225; 1-66.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA. IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 71
SQ SEQUENCE 71 AA; 8179 MW; CE411588EB96209F CRC64;

Query Match 55.0%; Score 11; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11
DB 47 YGRKKRRQRRR 57

RESULT 10
O40226_9HIV1 PRELIMINARY; PRT; 71 AA.
AC O40226_
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=BT94-A2tat;
RC MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RX Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
and tat1 genes derived from individuals with different rates of
disease progression.";
RL Virology 232:319-331(1997).
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-----
CC EMBL; AF000524; AAB62523.1; -; Genomic_DNA.
DR HSSP; P04610; 1JFW.
DR SMR; O40226; 1-71.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.

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DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
FT NON_TER 71
SQ SEQUENCE 71 AA; 8337 MW; 50B9632849586A2C CRC64;

Query Match 55.0%; Score 11; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11
DB 47 YGRKKRRQRRR 57

RESULT 11
O40227_9HIV1
ID O40227_9HIV1 PRELIMINARY; PRT; 71 AA.
AC O40227;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CH94-A2tat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RA "Activity of human immunodeficiency virus type 1 promoter/TAR regions
and tat1 genes derived from individuals with different rates of
disease progression.";
RL Virology 232:319-331 (1997).
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-----
DR EMBL; AF000525; AAB62524.1; -; Genomic_DNA.
DR HSSP; P04610; 1JFW.
DR SMR; O40227; 1-71.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8247 MW; C880BD85C90230B5 CRC64;

Query Match 55.0%; Score 11; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11
DB 47 YGRKKRRQRRR 57

RESULT 12
O40228_9HIV1
ID O40228_9HIV1 PRELIMINARY; PRT; 71 AA.
AC O40228;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HE93-A3tat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RA "Activity of human immunodeficiency virus type 1 promoter/TAR regions
and tat1 genes derived from individuals with different rates of
disease progression.";
RL Virology 232:319-331 (1997).
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-----
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DJ91-altat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RA "Activity of human immunodeficiency virus type 1 promoter/TAR regions
and tat1 genes derived from individuals with different rates of
disease progression.";
RL Virology 232:319-331 (1997).
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-----
DR EMBL; AF000526; AAB62525.1; -; Genomic_DNA.
DR HSSP; P04610; 1JFW.
DR SMR; O40228; 1-71.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8191 MW; C880A34AEAFF30E5 CRC64;

Query Match 55.0%; Score 11; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRR 11
DB 47 YGRKKRRQRRR 57

RESULT 13
O40231_9HIV1
ID O40231_9HIV1 PRELIMINARY; PRT; 71 AA.
AC O40231;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HE93-A3tat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RA "Activity of human immunodeficiency virus type 1 promoter/TAR regions
and tat1 genes derived from individuals with different rates of
disease progression.";
RL Virology 232:319-331 (1997).
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CC -----
DR EMBL; AF000529; AAB62528.1; -; Genomic_DNA.
DR HSP; P04610; 1JFW.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8162 MW; 5AF3242882321B3 CRC64;

Query Match 55.0%; Score 11; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
Db 47 YGRKKRQRRR 57

RESULT 14
O40232_9HIV1 PRELIMINARY; PRT; 71 AA.
AC O40232.
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Tat protein (Fragment).
DE Name:tat;
GN Name:tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HP91-Altat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
RT and tat1 genes derived from individuals with different rates of
RT disease progression.";
RL Virology 232:319-331(1997).
CC -----
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CC -----
DR EMBL; AF000530; AAB62529.1; -; Genomic_DNA.
DR HSP; P04610; 1JFW.
DR SMR; O40232; 1-71.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8226 MW; 324F908AF030E216 CRC64;

Query Match 55.0%; Score 11; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
Db 47 YGRKKRQRRR 57

RESULT 15
O40233_9HIV1 PRELIMINARY; PRT; 71 AA.
ID O40233.
AC O40233.
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Tat protein (Fragment).
DE Name:tat;
GN Name:tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MR94-A3tat;
RX MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
RT and tat1 genes derived from individuals with different rates of
RT disease progression.";
RL Virology 232:319-331(1997).
CC -----
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CC -----
DR EMBL; AF000531; AAB62530.1; -; Genomic_DNA.
DR HSP; P12506; 1TBC.
DR SMR; O40233; 1-71.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8034 MW; 5BBA79FB327EA3CD CRC64;

Query Match 55.0%; Score 11; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRQRRR 11
Db 47 YGRKKRQRRR 57

Search completed: August 24, 2006, 23:51:26
Job time : 301 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:42:38 ; Search time 197 Seconds  
(without alignments)  
46.418 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKKRQRRKRPASADGHR 20

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2581586

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_8.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	9	AED21152
2	12	60.0	12	4	AAB83294
3	12	60.0	12	4	AAB83295
4	12	60.0	20	8	ADO20689
5	12	60.0	20	8	ADO20727
6	12	60.0	20	8	ADO20723
7	12	60.0	20	8	ADO20599
8	12	60.0	20	8	ADO20674
9	12	60.0	20	8	ADO20697
10	12	60.0	20	8	ADO20730
11	12	60.0	20	8	ADU15784
12	12	60.0	20	9	AEBO7971
13	12	60.0	20	9	AEBO7972
14	12	60.0	20	9	AEBO7884
15	11	55.0	11	2	AAW50263
16	11	55.0	11	2	AAV05415
17	11	55.0	11	2	AAV25075
18	11	55.0	11	3	AAAB27088
19	11	55.0	11	3	AAAB09907
20	11	55.0	11	3	AAV93542
21	11	55.0	11	3	AAV71015
22	11	55.0	11	3	AAAB35698
23	11	55.0	11	3	AAAB03961

ALIGNMENTS

RESULT 1				
AED21152				
ID	AED21152	standard; peptide; 20 AA.		
XX	AC	AED21152;		
XX	AC			
DT	01-DEC-2005	(first entry)		
DE	SUDAPI-1/ HIV Tat domain fusion peptide, TSUDAPI-1 SEQ ID NO: 2.			
XX				
KW	Protein interaction; therapeutic; cerebrovascular ischemia;			
KW	cerebroprotective; vasotropic; hypoxia; ischemia; multiple sclerosis;			
KW	neuroprotective; Huntingtons chorea; anticonvulsant; nootropic;			
KW	parkinsons disease; antiparkinsonian; alzheimers disease; hyperglycemia;			
KW	antidiabetic; diabetes; trauma; tranquilizer; vulnerary; epilepsy;			
KW	grand mal seizure; muscle hypertonia; muscle relaxant; paralysis;			
KW	muscular-gen.; asthma; antiasthmatic; cardiac arrest; cardiac;			
KW	macular degeneration; ophthalmological; psychiatric disorder;			
KW	neuroleptic; schizophrenia; AIDS dementia complex; dementia;			
KW	inflammation; antiinflammatory; pain; analgesic; opiate dependence;			
KW	antiaddictive; cocaine addiction; alcoholism; antialcoholic;			
KW	anorexia nervosa; anabolic; eating-disorders-gen.;			
KW	Src-unique domain anchoring protein inhibitor.			
XX	Homo sapiens.			
OS	Human immunodeficiency virus.			
XX				
FH	Key	Location/Qualifiers		
FT	Region	1..11		
FT	Region	/note= "HIV transduction domain (TAT)"		
FT	Region	12..20		
XX		/note= "Src unique domain anchoring protein inhibitor 1"		
XX	US2005222042-A1.			
PN	06-OCT-2005.			
XX				
XX	30-MAR-2004; 2004US-00814109.			
PR	30-MAR-2004; 2004US-00814109.			
XX	(HOSP-) HOSPITAL FOR SICK CHILDREN RES INST.			
PA				
XX	Salter MW, Gingrich JR;			
XX	WPI; 2005-689427/71.			
DR				

Aab29413 HIV Tat t  
Aab03932 TAT prote  
Aab71757 HIV Tat p  
Aab71756 NTR3 deri  
Aab60006 Internali  
Aae05268 Human imm  
Aae02973 Protein t  
Aae03418 Human imm  
Aab03815 HIV tat p  
Aab98683 HIV Tat p  
Aab73305 HIV-1 TAT  
Aag70458 Human G2  
Aag68376 Human Ck  
Aae65673 HIV tat p  
Aae12605 Human imm  
Aab67673 Transduct  
Aae03730 Protein t  
Aam50221 HIV-1 tat  
Aau09932 Human imm  
Aae12891 Human imm  
Aae13064 Protein t  
Aab69170 HIV tat p

24 11 55.0 11 3 AAB29413  
25 11 55.0 11 3 AAB03932  
26 11 55.0 11 4 AAB71757  
27 11 55.0 11 4 AAB71756  
28 11 55.0 11 4 AAB60006  
29 11 55.0 11 4 AAE05268  
30 11 55.0 11 4 AAE02973  
31 11 55.0 11 4 AAE03418  
32 11 55.0 11 4 AAB03815  
33 11 55.0 11 4 AAB98683  
34 11 55.0 11 4 AAB73305  
35 11 55.0 11 4 AAG70458  
36 11 55.0 11 4 AAG68376  
37 11 55.0 11 4 AAE65673  
38 11 55.0 11 4 AAE12605  
39 11 55.0 11 4 AAB67673  
40 11 55.0 11 4 AAE03730  
41 11 55.0 11 4 AAM50221  
42 11 55.0 11 4 AAU09932  
43 11 55.0 11 4 AAE12891  
44 11 55.0 11 4 AAE13064  
45 11 55.0 11 4 AAB69170

XX Modifying N-methyl-D-aspartate receptor interaction with non-receptor  
PT tyrosine kinase Src in cells, comprises administering composition  
PT comprising Src-unique domains anchoring protein inhibitor to cells.  
XX  
XX  
PS Claim 13; SEQ ID NO 2; 32pp; English.  
XX  
XX The present invention provides a method for modifying N-methyl-D-  
CC aspartate receptor (NMDAR) interaction with non-receptor tyrosine kinase  
CC Src in cells. The method involves administering a composition including  
CC at least one Src-unique domain anchoring protein inhibitor (SUDAPI) to  
CC the cells, where modification ameliorates a disease or condition related  
CC to NMDAR signaling. Diseases or conditions ameliorated by the invention  
CC include stroke, hypoxia, ischemia, multiple sclerosis, Huntington's  
CC chorea, Parkinson's disease, Alzheimer's disease, hyperglycemia,  
CC diabetes, traumatic injury, epilepsy, grand mal seizures, spasticity,  
CC cerebral palsy, asthma, cardiac arrest, macular degeneration, mental  
CC diseases, schizophrenia, AIDS dementia complex, other dementias, AIDS  
CC wasting syndrome, inflammation, pain, opioid addiction, cocaine addiction,  
CC alcohol addiction and other conditions associated with substance abuse  
CC and anorexia. The present sequence is the SUDAPI-1/HIV Tat domain fusion  
CC peptide, TSUDAPI-1.  
XX  
XX Sequence 20 AA;  
SQ  
Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.6e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YGRKKRQRRRKPSADGHR 20  
DB 1 YGRKKRQRRRKPSADGHR 20  
RESULT 2  
AAB83294  
ID AAB83294 standard; peptide; 12 AA.  
XX  
AC AAB83294;  
XX  
XX 13-JUL-2001 (first entry)  
DT  
DE BBB peptide #1.  
XX  
XX Pulmonary delivery; bioconjugation; pulmonary fluid protein; opioid;  
KW systemic drug delivery; antihistamine; anti-angina; anti-hypertensive;  
KW anti-arrhythmic; anti-depressant; bronchodilator; anti-inflammatory;  
KW anti-thyroid deficiency; BBB.  
XX  
OS Synthetic.  
XX  
XX WO200117568-A2.  
PN  
XX 15-MAR-2001.  
PD  
XX 07-SEP-2000; 2000WO-IB001429.  
PP  
XX 07-SEP-1999; 99US-0152681P.  
PR  
XX (CONJ-) CONJUCHEM INC.  
PA  
XX Ezrin AM, Fleser A, Robitaille M, Milner PG, Bridon DP;  
PI  
XX WPI; 2001-354657/37.  
DR  
XX Pulmonary delivery of therapeutic agents which are capable of forming  
PT covalent bonds with amino, hydroxyl or thiol groups on pulmonary or blood  
PT components.  
XX  
XX Example 14; Page 139; 184pp; English.  
PS  
XX The present invention describes a modified therapeutic agent comprising a  
CC therapeutic agent and a reactive group which reacts with groups on  
CC pulmonary or blood components to form a stable covalent bond, where the  
CC therapeutic agent may be a peptide. Pulmonary drug delivery is useful as  
CC it increases the drug retention-time in the lungs and reduces the risk of  
CC extrapulmonary side effects. Modified therapeutic agents of this type may  
CC be antihistamines, anti-angina, anti-hypertensive or anti-arrhythmic  
CC agents, anti-depressants, bronchodilators, opioids or their analogues,  
CC anti-inflammatory agents, or anti-thyroid deficiency agents. The present  
CC sequence is a BBB peptide  
XX  
XX Sequence 12 AA;  
SQ  
Query Match 60.0%; Score 12; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YGRKKRQRRRK 12  
DB 1 YGRKKRQRRRK 12  
RESULT 3  
AAB83295  
ID AAB83295 standard; peptide; 12 AA.  
XX  
XX AAB83295;  
AC  
XX 13-JUL-2001 (first entry)  
DT  
XX BBB peptide #2.  
DE  
XX Pulmonary delivery; bioconjugation; pulmonary fluid protein; opioid;  
KW systemic drug delivery; antihistamine; anti-angina; anti-hypertensive;  
KW anti-arrhythmic; anti-depressant; bronchodilator; anti-inflammatory;  
KW anti-thyroid deficiency; BBB.  
XX  
OS Synthetic.  
XX  
XX WO200117568-A2.  
PN  
XX 15-MAR-2001.  
PD  
XX 07-SEP-2000; 2000WO-IB001429.  
PP  
XX 07-SEP-1999; 99US-0152681P.  
PR  
XX (CONJ-) CONJUCHEM INC.  
PA  
XX Ezrin AM, Fleser A, Robitaille M, Milner PG, Bridon DP;  
PI  
XX WPI; 2001-354657/37.  
DR  
XX Pulmonary delivery of therapeutic agents which are capable of forming  
PT covalent bonds with amino, hydroxyl or thiol groups on pulmonary or blood  
PT components.  
XX  
XX Example 15; Page 141; 184pp; English.  
PS  
XX The present invention describes a modified therapeutic agent comprising a  
CC therapeutic agent and a reactive group which reacts with groups on  
CC pulmonary or blood components to form a stable covalent bond, where the  
CC therapeutic agent may be a peptide. Pulmonary drug delivery is useful as  
CC it increases the drug retention-time in the lungs and reduces the risk of  
CC extrapulmonary side effects. Modified therapeutic agents of this type may  
CC be antihistamines, anti-angina, anti-hypertensive or anti-arrhythmic  
CC agents, anti-depressants, bronchodilators, opioids or their analogues,  
CC anti-inflammatory agents, or anti-thyroid deficiency agents. The present  
CC sequence is a BBB peptide  
XX  
XX Sequence 12 AA;  
SQ  
Query Match 60.0%; Score 12; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC pulmonary or blood components to form a stable covalent bond, where the  
CC therapeutic agent may be a peptide. Pulmonary drug delivery is useful as  
CC it increases the drug retention-time in the lungs and reduces the risk of  
CC extrapulmonary side effects. Modified therapeutic agents of this type may  
CC be antihistamines, anti-angina, anti-hypertensive or anti-arrhythmic  
CC agents, anti-depressants, bronchodilators, opioids or their analogues,  
CC anti-inflammatory agents, or anti-thyroid deficiency agents. The present  
CC sequence is a BBB peptide  
XX  
XX Sequence 12 AA;  
SQ  
Query Match 60.0%; Score 12; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YGRKKRQRRRK 12  
DB 1 YGRKKRQRRRK 12  
RESULT 3  
AAB83295  
ID AAB83295 standard; peptide; 12 AA.  
XX  
XX AAB83295;  
AC  
XX 13-JUL-2001 (first entry)  
DT  
XX BBB peptide #2.  
DE  
XX Pulmonary delivery; bioconjugation; pulmonary fluid protein; opioid;  
KW systemic drug delivery; antihistamine; anti-angina; anti-hypertensive;  
KW anti-arrhythmic; anti-depressant; bronchodilator; anti-inflammatory;  
KW anti-thyroid deficiency; BBB.  
XX  
OS Synthetic.  
XX  
XX WO200117568-A2.  
PN  
XX 15-MAR-2001.  
PD  
XX 07-SEP-2000; 2000WO-IB001429.  
PP  
XX 07-SEP-1999; 99US-0152681P.  
PR  
XX (CONJ-) CONJUCHEM INC.  
PA  
XX Ezrin AM, Fleser A, Robitaille M, Milner PG, Bridon DP;  
PI  
XX WPI; 2001-354657/37.  
DR  
XX Pulmonary delivery of therapeutic agents which are capable of forming  
PT covalent bonds with amino, hydroxyl or thiol groups on pulmonary or blood  
PT components.  
XX  
XX Example 15; Page 141; 184pp; English.  
PS  
XX The present invention describes a modified therapeutic agent comprising a  
CC therapeutic agent and a reactive group which reacts with groups on  
CC pulmonary or blood components to form a stable covalent bond, where the  
CC therapeutic agent may be a peptide. Pulmonary drug delivery is useful as  
CC it increases the drug retention-time in the lungs and reduces the risk of  
CC extrapulmonary side effects. Modified therapeutic agents of this type may  
CC be antihistamines, anti-angina, anti-hypertensive or anti-arrhythmic  
CC agents, anti-depressants, bronchodilators, opioids or their analogues,  
CC anti-inflammatory agents, or anti-thyroid deficiency agents. The present  
CC sequence is a BBB peptide  
XX  
XX Sequence 12 AA;  
SQ  
Query Match 60.0%; Score 12; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 YGRKKRRQRRRK 12
Db      1 YGRKKRRQRRRK 12

RESULT 4
ADO20689
ID      ADO20689 standard; peptide; 20 AA.
AC      ADO20689;
XX
DT      26-AUG-2004 (first entry)
XX
DE      PSD-95 PDZ domain binding peptide #31.
XX
KW      neuroprotective; gene therapy; N-methyl-D-aspartate receptor;
KW      NMDA receptor; PDZ domain; PDZ protein; binding inhibitor;
KW      neuronal disorder; stroke; ischaemia; PSD-95; PDZ domain.
XX
OS      Unidentified.
XX
PN      WO2004045535-A2.
XX
PD      03-JUN-2004.
XX
PF      14-NOV-2003; 2003WO-US036698.
XX
PR      14-NOV-2002; 2002US-0426212P.
XX
PR      14-NOV-2002; 2002US-0426213P.
XX
PA      (ARBO-) ARBOR VITA CORP.
XX
PI      Lu PS, Garman JD, Belmares MP;
XX
DR      WPI; 2004-420526/39.
XX
PT      New pharmaceutical composition comprising a polypeptide that inhibits
PT      binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein,
PT      useful in treating a neuronal disorder e.g. an injury caused by stroke or
PT      ischemia.
XX
PS      Example 9; Page 105; 146pp; English.
XX
CC      The invention describes a pharmaceutical composition comprising an
CC      isolated, recombinant or synthetic polypeptide that inhibits binding
CC      between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a
CC      carrier, diluent or excipient and that comprises a C-terminal amino acid
CC      sequence of X-Thr-X-Val/Leu/Ala. Also described are: an isolated,
CC      recombinant or synthetic polypeptide for use in therapy and that
CC      comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and
CC      inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ
CC      protein; and a method for determining whether a test compound inhibits
CC      binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor.
CC      The pharmaceutical composition is useful in treating a neuronal disorder,
CC      which is an injury caused by stroke or ischaemia. This is the amino acid
CC      sequence of a PDZ domain ligand that binds to the PDZ domain of PSD-95.
XX
SQ      Sequence 20 AA;

Query Match      60.0%; Score 12; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YGRKKRRQRRRK 12
Db      1 YGRKKRRQRRRK 12

RESULT 6
ADO20723
ID      ADO20723 standard; peptide; 20 AA.
XX
AC      ADO20723;
XX
DT      26-AUG-2004 (first entry)
XX
DE      PSD-95 PDZ domain binding peptide #65.
XX
KW      neuroprotective; gene therapy; N-methyl-D-aspartate receptor;
KW      NMDA receptor; PDZ domain; PDZ protein; binding inhibitor;
KW      neuronal disorder; stroke; ischaemia; PSD-95; PDZ domain.
XX
XX

```



PT useful in treating a neuronal disorder e.g. an injury caused by stroke or  
 PT ischemia.

XX Example 9; Page 104; 146pp; English.

XX The invention describes a pharmaceutical composition comprising an  
 CC isolated, recombinant or synthetic polypeptide that inhibits binding  
 CC between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a  
 CC carrier, diluent or excipient and that comprises a C-terminal amino acid  
 CC sequence of X-Thr-X-Val/Leu/Ala. Also described are: an isolated,  
 CC recombinant or synthetic polypeptide for use in therapy and that  
 CC comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and  
 CC inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ  
 CC protein; and a method for determining whether a test compound inhibits  
 CC binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor.  
 CC The pharmaceutical composition is useful in treating a neuronal disorder,  
 CC which is an injury caused by stroke or ischaemia. This is the amino acid  
 CC sequence of a PDZ domain ligand that binds to the PDZ domain of PSD-95.  
 XX

SQ Sequence 20 AA;

Query Match 60.0%; Score 12; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.00022;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRK 12  
 |||||  
 Db 1 YGRKKRRQRRRK 12

RESULT 9

ADO20697  
 ID ADO20697 standard; peptide; 20 AA.

XX ADO20697;

XX 26-AUG-2004 (first entry)

XX PSD-95 PDZ domain binding peptide #39.

XX neuroprotective; gene therapy; N-methyl-D-aspartate receptor;  
 KW NMDA receptor; PDZ domain; PDZ protein; binding inhibitor;  
 KW neuronal disorder; stroke; ischaemia; PSD-95; PDZ domain.

XX Unidentified.

XX WO2004045535-A2.

XX 03-JUN-2004.

XX 14-NOV-2003; 2003WO-US036698.

XX 14-NOV-2002; 2002US-0426212P.

XX 14-NOV-2002; 2002US-0426213P.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS, Garman JD, Belmares MP;

XX WPI; 2004-420526/39.

XX New pharmaceutical composition comprising a polypeptide that inhibits  
 PT binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein,  
 PT useful in treating a neuronal disorder e.g. an injury caused by stroke or  
 PT ischemia.

XX Example 9; Page 105; 146pp; English.

XX The invention describes a pharmaceutical composition comprising an  
 CC isolated, recombinant or synthetic polypeptide that inhibits binding  
 CC between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a  
 CC carrier, diluent or excipient and that comprises a C-terminal amino acid  
 CC sequence of X-Thr-X-Val/Leu/Ala. Also described are: an isolated,  
 CC

CC recombinant or synthetic polypeptide for use in therapy and that  
 CC comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and  
 CC inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ  
 CC protein; and a method for determining whether a test compound inhibits  
 CC binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor.  
 CC The pharmaceutical composition is useful in treating a neuronal disorder,  
 CC which is an injury caused by stroke or ischaemia. This is the amino acid  
 CC sequence of a PDZ domain ligand that binds to the PDZ domain of PSD-95.  
 XX

SQ Sequence 20 AA;

Query Match 60.0%; Score 12; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.00022;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRK 12  
 |||||  
 Db 1 YGRKKRRQRRRK 12

RESULT 10

ADO20730

ID ADO20730 standard; peptide; 20 AA.

XX ADO20730;

XX 26-AUG-2004 (first entry)

XX PSD-95 PDZ domain binding peptide #72.

XX neuroprotective; gene therapy; N-methyl-D-aspartate receptor;  
 KW NMDA receptor; PDZ domain; PDZ protein; binding inhibitor;  
 KW neuronal disorder; stroke; ischaemia; PSD-95; PDZ domain.

XX Unidentified.

XX WO2004045535-A2.

XX 03-JUN-2004.

XX 14-NOV-2003; 2003WO-US036698.

XX 14-NOV-2002; 2002US-0426212P.

XX 14-NOV-2002; 2002US-0426213P.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS, Garman JD, Belmares MP;

XX WPI; 2004-420526/39.

XX New pharmaceutical composition comprising a polypeptide that inhibits  
 PT binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein,  
 PT useful in treating a neuronal disorder e.g. an injury caused by stroke or  
 PT ischemia.

XX Example 9; Page 105; 146pp; English.

XX The invention describes a pharmaceutical composition comprising an  
 CC isolated, recombinant or synthetic polypeptide that inhibits binding  
 CC between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a  
 CC carrier, diluent or excipient and that comprises a C-terminal amino acid  
 CC sequence of X-Thr-X-Val/Leu/Ala. Also described are: an isolated,  
 CC recombinant or synthetic polypeptide for use in therapy and that  
 CC comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and  
 CC inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ  
 CC protein; and a method for determining whether a test compound inhibits  
 CC binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor.  
 CC The pharmaceutical composition is useful in treating a neuronal disorder,  
 CC which is an injury caused by stroke or ischaemia. This is the amino acid  
 CC sequence of a PDZ domain ligand that binds to the PDZ domain of PSD-95.  
 XX

SQ Sequence 20 AA;

```

Query Match      60.0%; Score 12; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRK 12
   |||||
DB 1 YGRKKRRQRRRK 12

RESULT 11
ADU15784
ID ADU15784 standard; peptide; 20 AA.
XX
AC ADU15784;
XX
DT 13-JAN-2005 (first entry)
XX
DE MUC1-PDZ domain binding inhibitor transmembrane transporter peptide #66.
XX
KW cytoplasmic domain; MUC1; PDZ domain; transmembrane transporter.
XX
OS Human immunodeficiency virus 1.
XX
PN WO2004092339-A2.
XX
PD 28-OCT-2004.
XX
PF 12-APR-2004; 2004WO-US011195.
XX
PR 11-APR-2003; 2003US-0462111P.
PR 02-MAY-2003; 2003US-0467728P.
PR 04-JUN-2003; 2003US-0475595P.
PR 11-SEP-2003; 2003US-0502111P.
PR 21-NOV-2003; 2003US-0524188P.
XX
XX (ILEX-) ILEX PROD INC.
PA (ARBO-) ARBOR VITA CORP.
PA (DAND ) DANA FARBBER CANCER INST.
XX
XX Belmares MP, Lu PS, Garman JD, Jecminek AA, Kharbanda S, Agata N;
PI Kufe DW;
XX
XX WPI; 2004-766852/75.
XX
XX Inhibiting the binding of the cytoplasmic domain of MUC1 to a PDZ domain,
PT comprises contacting the PDZ domain with an agent that competes with the
PT binding of the C-terminal region of the cytoplasmic domain of MUC1 with
PT the PDZ domain.
XX
XX Disclosure; SEQ ID NO 168; 141pp; English.
XX
XX The invention relates to a method of inhibiting the binding of the
CC cytoplasmic domain of MUC1 to a PDZ domain, by contacting the PDZ domain
CC with an effective amount of an agent that competes with the binding of
CC the C-terminal region of the cytoplasmic domain of MUC1 with the PDZ
CC domain. The PDZ domain is 20-1 d2, S1P1 d1, LIM MISTIQUE, AIPC, KIAA0751,
CC NAST2, PRIL-16 d1, GRIP2 d5, SITAC 18, NSP or KIAA1526 d1. The agent that
CC competes with binding of the C-terminal region of cytoplasmic domain of
CC MUC1 with the PDZ domain is a peptide of the formula (I): X1-aa2-aa1-aa0,
CC where aa0 is a hydrophobic aliphatic amino acid residue or a hydrophobic
CC aromatic amino acid residue; aa2 is a hydrophobic aliphatic amino acid
CC residue, hydrophobic aromatic amino acid residue, polar amino acid
CC residue, basic amino acid residue or an acidic amino acid residue; aa1 is
CC any amino acid residue; and X1 is a sequence of 0-50 amino acid residues.
CC Preferably aa2-aa1-aa0 is selected from SEQ ID NO: 1-40 (ADU15617-
CC ADU15656) and X1 may be selected from SEQ ID NO: 41-94 (ADU15657-
CC ADU15710). The method is useful for inhibiting the binding of the
CC cytoplasmic domain of MUC1 to a PDZ domain. The amino terminal of the X1
CC peptide may also contain a transmembrane transporter peptide. The
CC transporter sequence may be selected from SEQ ID NO: 97-127 (ADU15713-
CC ADU15743). This peptide is derived from the HIV transactivator (TAT)
CC protein.

```

```

XX
SQ Sequence 20 AA;
XX
XX Query Match      60.0%; Score 12; DB 8; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 0.00022;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YGRKKRRQRRRK 12
XX   |||||
XX DB 1 YGRKKRRQRRRK 12
XX
XX RESULT 12
XX AEB07971
XX ID AEB07971 standard; peptide; 20 AA.
XX
XX AC AEB07971;
XX
XX DT 08-SEP-2005 (first entry)
XX
XX DE Peptide binding to PAR3 PDZ domain 3 SEQ ID 363.
XX
XX KW Protein interaction; protein therapy;
XX KW transient receptor potential channel; TRP; cell death; PDZ domain;
XX KW Vasotrophic; Nootropic; Neuroprotective; Ophthalmological;
XX KW Antiparkinsonian; Anticonvulsant; cerebroprotective; vulnerary; cardiant;
XX KW muscular-gen.; cns-gen.; brain injury; spinal cord injury; ischemia;
XX KW trauma; degeneration; cerebrovascular ischemia; epilepsy;
XX KW Parkinsons disease; glaucoma; Alzheimer's disease; myocardial ischemia;
XX KW Huntingtons chorea; ataxia; motor neurone disease.
XX
XX OS Synthetic.
XX
XX PN WO2005061548-A1.
XX
XX PD 07-JUL-2005.
XX
XX PF 22-DEC-2004; 2004WO-CA002193.
XX
XX PR 23-DEC-2003; 2003US-0532169P.
XX
XX PA (ARBO-) ARBOR VITA CORP.
XX PA (NONO-) NONO INC.
XX
XX PI Tymianski M, Garman JD, Belmares MP;
XX
XX DR WPI; 2005-479449/48.
XX
XX PT New isolated polypeptides inhibiting binding between a transient receptor
PT potential (TRP) channel protein and a TRP-associated protein, useful in
PT reducing damage to mammalian cells following stroke, epilepsy or spinal
PT cord injuries.
XX
XX Example 3; SEQ ID NO 363; 377pp; English.
XX
XX The invention relates to an inhibitor comprising an isolated, recombinant
CC or synthetic polypeptide that inhibits binding between a transient
CC receptor potential (TRP) channel protein and a TRP-associated protein
CC (e.g. one containing a PDZ domain). Also included are a pharmaceutical
CC composition comprising the inhibitor cited above (and a physiological
CC carrier, diluent or excipient), an inhibitor comprising a nucleic acid
CC sequence capable of inhibiting the expression of a TRP channel protein
CC post transcriptionally, treating mammalian cell injury (comprising
CC introducing a modulator of binding between a TRP channel protein and a
CC TRP channel associated protein into a cell), reducing the damaging effect
CC of ischemia/traumatic injury to the brain/spinal cord in a mammal
CC (comprising treating the mammal with a non-toxic, damage-reducing,
CC effective amount of a modulator of binding between a TRP channel protein
CC and a TRP channel associated protein), controlling the concentration of
CC Ca2+ -dependent signaling molecules in the vicinity of ion channel pores
CC of cells in vivo (to prevent the diffusion of toxic amounts of the Ca2+
CC influx) to prevent the triggering of neurotoxic phenomena (comprising
CC administering an effective, non-toxic amount of a modulator of TRP

```



channel proteins or cellular protein interaction domains that effect the TRP channel protein interactions) and determining whether a test compound modulates binding between a TRP channel protein and a PDZ domain-containing polypeptide (comprising contacting a TRP channel PDZ-Ligand sequence with a PDZ domain-containing polypeptide, and measuring the amount of complex formed between the TRP channel PDZ-Ligand sequence and the PDZ domain-containing polypeptide). The TRP-associated protein in the inhibitor cited above comprises at least one PDZ domain selected from RIM -2, Mint 1, INADL, Syntrophin 1 alpha, SITAC-18, LIM mystique, ZO-1, PAR3L, MAST2, PARS, and novel serine protease. The TRP channel protein is human TRPM7 or mouse TRPM7. The methods and compositions of the present invention are useful for reducing the damaging effect of an injury to mammalian cells, including brain and spinal cord cells, by treatment with compounds which reduce cell death or dysfunction, including cellular damage following episodes of tissue ischemia and trauma. Also treatable with the methods and compositions and acute or chronic degeneration, such as in stroke, epilepsy, Parkinson's disease, glaucoma, Alzheimer's disease, spinal cord injuries, myocardial ischemia, Huntington's chorea, inherited ataxias and motor neurone disease. The present sequence is a peptide tested for its ability to bind to a selected PDZ domain or inhibit the binding of the PDZ domain to a TRP protein.

Sequence 20 AA;

Query Match 60.0%; Score 12; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKKRRQRRRK 12

DB 1 YGKKRRQRRRK 12

RESULT 13

AEBO7972

ID AEBO7972 standard; peptide; 20 AA.

AC AEBO7972;

DT 08-SEP-2005 (first entry)

DE Peptide binding to RIM2 PDZ domain 1 SEQ ID 364.

Protein interaction; protein therapy;  
transient receptor potential channel; TRP; cell death; PDZ domain;  
Vasotrophic; Nootropic; Neuroprotective; Ophthalmological;  
Antiparkinsonian; Anticonvulsant; cerebroprotective; vulnerary; cardiant;  
muscular-gen.; cns-gen.; brain injury; spinal cord injury; ischemia;  
trauma; degeneration; cerebrovascular ischemia; epilepsy;  
Parkinsons disease; glaucoma; Alzheimer's disease; myocardial ischemia;  
Huntingtons chorea; ataxia; motor neurone disease.

OS Synthetic.

FN WO2005061548-A1.

PD 07-JUL-2005.

PF 22-DEC-2004; 2004WO-CA002193.

PR 23-DEC-2003; 2003US-0532169P.

PA (ARBO-) ARBOR VITA CORP.  
PA (NONO-) NONO INC.

PI Tymianski M, Garman JD, Belmares MP;

XX WPI; 2005-479449/48.

New isolated polypeptides inhibiting binding between a transient receptor potential (TRP) channel protein and a TRP-associated protein, useful in reducing damage to mammalian cells following stroke, epilepsy or spinal cord injuries.

XX Example 3; SEQ ID NO 364; 377pp; English.

The invention relates to an inhibitor comprising an isolated, recombinant or synthetic polypeptide that inhibits binding between a transient receptor potential (TRP) channel protein and a TRP-associated protein (e.g. one containing a PDZ domain). Also included are a pharmaceutical composition comprising the inhibitor cited above (and a physiological carrier, diluent or excipient), an inhibitor comprising a nucleic acid sequence capable of inhibiting the expression of a TRP channel protein post transcriptionally, treating mammalian cell injury (comprising introducing a modulator of binding between a TRP channel protein and a TRP channel associated protein into a cell), reducing the damaging effect of ischemia/traumatic injury to the brain/spinal cord in a mammal (comprising treating the mammal with a non-toxic, damage-reducing, effective amount of a modulator of binding between a TRP channel protein and a TRP channel associated protein), controlling the concentration of Ca2+-dependent signaling molecules in the vicinity of ion channel pores of cells in vivo (to prevent the diffusion of toxic amounts of the Ca2+ influx) to prevent the triggering of neurotoxic phenomena (comprising administering an effective, non-toxic amount of a modulator of TRP channel proteins or cellular protein interaction domains that effect the TRP channel protein interactions) and determining whether a test compound modulates binding between a TRP channel protein and a PDZ domain-containing polypeptide (comprising contacting a TRP channel PDZ-Ligand sequence with a PDZ domain-containing polypeptide, and measuring the amount of complex formed between the TRP channel PDZ-Ligand sequence and the PDZ domain-containing polypeptide). The TRP-associated protein in the inhibitor cited above comprises at least one PDZ domain selected from RIM -2, Mint 1, INADL, Syntrophin 1 alpha, SITAC-18, LIM mystique, ZO-1, PAR3L, MAST2, PARS, and novel serine protease. The TRP channel protein is human TRPM7 or mouse TRPM7. The methods and compositions of the present invention are useful for reducing the damaging effect of an injury to mammalian cells, including brain and spinal cord cells, by treatment with compounds which reduce cell death or dysfunction, including cellular damage following episodes of tissue ischemia and trauma. Also treatable with the methods and compositions and acute or chronic degeneration, such as in stroke, epilepsy, Parkinson's disease, glaucoma, Alzheimer's disease, spinal cord injuries, myocardial ischemia, Huntington's chorea, inherited ataxias and motor neurone disease. The present sequence is a peptide tested for its ability to bind to a selected PDZ domain or inhibit the binding of the PDZ domain to a TRP protein.

Sequence 20 AA;

Query Match 60.0%; Score 12; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKKRRQRRRK 12

DB 1 YGKKRRQRRRK 12

RESULT 14

AEBO7884

ID AEB07884 standard; peptide; 20 AA.

AC AEB07884;

DT 08-SEP-2005 (first entry)

DE Peptide inhibitor of TRPM7-ZO-1/INADL PDZ domains, 1852.

Protein interaction; protein therapy;  
transient receptor potential channel; TRP; cell death; PDZ domain;  
Vasotrophic; Nootropic; Neuroprotective; Ophthalmological;  
Antiparkinsonian; Anticonvulsant; cerebroprotective; vulnerary; cardiant;  
muscular-gen.; cns-gen.; brain injury; spinal cord injury; ischemia;  
trauma; degeneration; cerebrovascular ischemia; epilepsy;  
Parkinsons disease; glaucoma; Alzheimer's disease; myocardial ischemia;  
Huntingtons chorea; ataxia; motor neurone disease.

OS Synthetic.  
XX WO2005061548-A1.  
XX 07-JUL-2005.  
XX  
XX 22-DEC-2004; 2004WO-CA002193.  
XX  
XX 23-DEC-2003; 2003US-0532169P.  
XX  
XX (ARBO-) ARBOR VITA CORP.  
XX (NONO-) NONO INC.  
XX  
XX Tymianski M, Garman JD, Belmares MP;  
XX WPI; 2005-479449/48.  
XX  
XX New isolated polypeptides inhibiting binding between a transient receptor  
PT potential (TRP) channel protein and a TRP-associated protein, useful in  
PT reducing damage to mammalian cells following stroke, epilepsy or spinal  
PT cord injuries.  
XX  
XX Example 3; SEQ ID NO 276; 377pp; English.  
XX  
XX The invention relates to an inhibitor comprising an isolated, recombinant  
CC or synthetic polypeptide that inhibits binding between a transient  
CC receptor potential (TRP) channel protein and a TRP-associated protein  
CC (e.g. one containing a PDZ domain). Also included are a pharmaceutical  
CC composition comprising the inhibitor cited above (and a physiological  
CC carrier, diluent or excipient), an inhibitor comprising a nucleic acid  
CC sequence capable of inhibiting the expression of a TRP channel protein  
CC post transcriptionally, treating mammalian cell injury (comprising  
CC introducing a modulator of binding between a TRP channel protein and a  
CC TRP channel associated protein into a cell), reducing the damaging effect  
CC of ischemia/traumatic injury to the brain/spinal cord in a mammal  
CC (comprising treating the mammal with a non-toxic, damage-reducing,  
CC effective amount of a modulator of binding between a TRP channel protein  
CC and a TRP channel associated protein), controlling the concentration of  
CC Ca2+ -dependent signaling molecules in the vicinity of ion channel pores  
CC of cells in vivo (to prevent the diffusion of toxic amounts of the Ca2+  
CC influx) to prevent the triggering of neurotoxic phenomena (comprising  
CC administering an effective, non-toxic amount of a modulator of TRP  
CC channel proteins or cellular protein interaction domains that effect the  
CC TRP channel protein interactions) and determining whether a test compound  
CC modulates binding between a TRP channel protein and a PDZ domain-  
CC containing polypeptide (comprising contacting a TRP channel PDZ-ligand  
CC sequence with a PDZ domain-containing polypeptide, and measuring the  
CC amount of complex formed between the TRP channel PDZ-ligand sequence and  
CC the PDZ domain-containing polypeptide). The TRP-associated protein in the  
CC inhibitor cited above comprises at least one PDZ domain selected from RIM  
CC -2, Mint 1, INADL, Syntrophin 1 alpha, SIFAC-18, LIM mystique, ZO-1,  
CC PAR3L, MAST2, PARS, and novel serine protease. The TRP channel protein is  
CC human TRPM7 or mouse TRPM7. The methods and compositions of the present  
CC invention are useful for reducing the damaging effect of an injury to  
CC mammalian cells, including brain and spinal cord cells, by treatment with  
CC compounds which reduce cell death or dysfunction, including cellular  
CC damage following episodes of tissue ischemia and trauma. Also treatable  
CC with the methods and compositions and acute or chronic degeneration, such  
CC as in stroke, epilepsy, Parkinson's disease, glaucoma, Alzheimer's  
CC disease, spinal cord injuries, myocardial ischemia, Huntington's chorea,  
CC inherited ataxias and motor neurone disease. The present sequence is a  
CC peptide tested for its ability to bind to a selected PDZ domain or  
CC inhibit the binding of the PDZ domain to a TRP protein.  
XX  
XX Sequence 20 AA;

Query Match 60.0%; Score 12; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YGRKKRRQRRK 12  
Db 1 YGRKKRRQRRK 12

RESULT 15  
AAW50263 standard; protein; 11 AA.  
XX  
XX AAW50263;  
XX  
XX 17-OCT-2003 (revised)  
DT 20-JUL-1998 (first entry)  
XX  
XX HIV-1 tat protein.  
XX  
XX Mouse; BH3 interacting domain death agonist; BID; BCL-2 family;  
KW apoptosis; regulation; cell death; inflammation; cancer; arthritis;  
KW autoimmune disease; viral infection; lymphoproliferative.  
XX  
XX Human immunodeficiency virus 1.  
OS  
XX WO9809980-A1.  
PN  
XX 12-MAR-1998.  
PD  
XX 09-SEP-1997; 97WO-US015872.  
XX  
XX 09-SEP-1996; 96US-00706741.  
XX (UNIW ) UNIV WASHINGTON.  
XX  
XX Korsemeyer SJ;  
XX  
XX WPI; 1998-193546/17.  
XX  
XX BH3 interacting domain death agonist polypeptide - used for treating  
PT decreased apoptotic conditions resulting from inflammation etc.  
XX  
XX Example 8; Page 85; 118pp; English.  
XX  
XX The present sequence represents the HIV-1 tat protein which is used in an  
CC example of the present invention which describes a BH3 interacting domain  
CC death agonist (BID) truncated protein. The BID protein, the DNA encoding  
CC it or antisense sequences can be used for preventing or treating a  
CC decreased apoptotic state of a cell. The decreased apoptotic state that  
CC is treated results from a disease such as cancer, viral infections,  
CC lymphoproliferative conditions, arthritis, inflammation and autoimmune  
CC diseases. Antibodies against the BID protein can be used for detecting a  
CC BID polypeptide in a cell or population of cell. The nucleic acid  
CC sequence and the BID protein can also be used for treating  
CC immunodeficiency disease (including AIDS), senescence, neurodegenerative  
CC disease, ischaemic and reperfusion cell death, infertility and wound-  
CC healing. Primers derived from the nucleic acid encoding the BID protein  
CC can be used for detecting/quantitating the protein and for detecting  
CC alterations in the nucleic acid encoding the BID protein. (Updated on 17-  
CC OCT-2003 to standardise OS field)  
XX  
XX Sequence 11 AA;  
SQ  
Query Match 55.0%; Score 11; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YGRKKRRQRRR 11  
Db 1 YGRKKRRQRRR 11

Search completed: August 24, 2006, 23:46:23  
Job time : 200 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:29:16 ; Search time 299 Seconds  
(without alignments)  
61.874 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 107

Sequence: 1 YGKRRRRRRKPASADGHR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	75.7	101	2	Q3S5F8_9HIV1
2	80	74.8	101	2	Q5FXH8_9HIV1
3	80	74.8	101	2	Q6B4P4_9HIV1
4	80	74.8	101	2	Q8USZ0_9HIV1
5	79	73.8	101	2	Q3SP9_9HIV1
6	79	73.8	101	2	Q6X8H0_9HIV1
7	79	73.8	101	2	Q8QDF8_9HIV1
8	79	73.8	101	2	Q900L1_9HIV1
9	78	72.9	71	2	Q5UGB0_9HIV1
10	78	72.9	71	2	Q5UGB1_9HIV1
11	78	72.9	71	2	Q8ATV7_9HIV1
12	78	72.9	72	2	Q8UMM5_9HIV1
13	78	72.9	72	2	Q8UMM6_9HIV1
14	78	72.9	72	2	Q8UMM7_9HIV1
15	78	72.9	72	2	Q8UMM8_9HIV1
16	78	72.9	72	2	Q8UMM1_9HIV1
17	78	72.9	72	2	Q8UMM4_9HIV1
18	78	72.9	72	2	Q8UMM6_9HIV1
19	78	72.9	72	2	Q8UMM9_9HIV1
20	78	72.9	72	2	Q8UMM0_9HIV1
21	78	72.9	72	2	Q8UMM2_9HIV1
22	78	72.9	99	2	Q8UT76_9HIV1
23	78	72.9	101	2	Q90085_9HIV1
24	78	72.9	101	2	Q4USB2_9HIV1
25	78	72.9	101	2	Q5FXR6_9HIV1
26	78	72.9	101	2	Q5FXU2_9HIV1
27	78	72.9	101	2	Q6S808_9HIV1
28	78	72.9	101	2	Q6X6J5_9HIV1
29	78	72.9	101	2	Q6XG08_9HIV1
30	78	72.9	101	2	Q90CH6_9HIV1
31	78	72.9	101	2	Q90CY2_9HIV1

32 77 72.0 71 2 Q6GMR7\_9HIV1 human immun  
33 77 72.0 71 2 Q9IQM6\_9HIV1 human immun  
34 77 72.0 72 2 P90173\_9HIV1 human immun  
35 77 72.0 101 2 Q6S864\_9HIV1 human immun  
36 77 72.0 101 2 Q7SUX3\_9HIV1 human immun  
37 77 72.0 101 2 Q8UTR5\_9HIV1 human immun  
38 77 72.0 101 2 Q9OSS7\_9HIV1 human immun  
39 76 71.0 71 2 Q71898\_9HIV1 human immun  
40 76 71.0 71 2 Q71905\_9HIV1 human immun  
41 76 71.0 71 2 Q71919\_9HIV1 human immun  
42 76 71.0 71 2 Q71926\_9HIV1 human immun  
43 76 71.0 71 2 Q71932\_9HIV1 human immun  
44 76 71.0 71 2 Q8ATW8\_9HIV1 human immun  
45 76 71.0 71 2 Q8ATY7\_9HIV1 human immun

## ALIGNMENTS

RESULT 1  
Q3S5F8\_9HIV1  
ID Q3S5F8\_9HIV1 PRELIMINARY; PRT; 101 AA.  
AC Q3S5F8; 2005, integrated into UniProtKB/TrEMBL.  
DT 11-OCT-2005, sequence version 1.  
DT 07-FEB-2006, entry version 4.  
DE Tat protein.  
GN Namestat;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=04ZAPS206B1;  
RA Birditt B.A., Rouseau C.M., Korber B.T., Goulder P., Brander C., Kiepiela P., Walker B.D., Mullins J.I.;  
RT "HIV HLA epitope mapping from Durban, South Africa";  
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC EMBL; DQ164126; AAZ91932.1; -; Genomic RNA.  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR GO; GO:0006350; P:transcription; IEA.  
DR InterPro; IPR001831; IV\_Tat.  
DR Pfam; PF00539; Tat; 1.  
DR PRINTS; PR00055; HIVTATDOMAIN.  
KW Activator; Nuclear protein; RNA-binding; Transcription;  
KW Transcription regulation.  
SQ SEQUENCE 101 AA; 11392 MW; F65CC51C6C0B25C3 CRC64;  
Query Match 75.7%; Score 81; DB 2; Length 101;  
Best Local Similarity 70.0%; Pred. No. 0.00045;  
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YGKRRRRRRKPASADGHR 20  
|||||||  
Db 47 YGKRRRRRRKPASADGHR 66  
RESULT 2  
Q5FXH8\_9HIV1  
ID Q5FXH8\_9HIV1 PRELIMINARY; PRT; 101 AA.  
AC Q5FXH8;  
DT 01-MAR-2005, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2005, sequence version 1.  
DT 07-FEB-2006, entry version 5.







```
ID QBATV7_9HIV1 PRELIMINARY; PRT; 71 AA.
AC QBATV7;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Tat protein (Fragment).
GN Name=cat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nanteza M.B., Yirell D.L., Kintu P., Kaleebu P., Biryahwaho B.,
RA Morgan D., Whitworth J.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AF425969; AAN31625.1; -; Genomic_DNA.
DR HSSP; P04613; 1K5K.
DR SMR; QBATV7: 1-71.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 71
SQ SEQUENCE 71 AA; 8243 MW; 3D10B9A460729AF2 CRC64;

Query Match 72.9%; Score 78; DB 2; Length 71;
Best Local Similarity 70.0%; Pred. No. 0.00087;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPASADGHR 20
DB 47 YGRKKRRQRRSPQSQAHQ 66

RESULT 12
QBUMM5_9HIV1 PRELIMINARY; PRT; 72 AA.
AC QBUMM5;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Tat protein (Fragment).
GN Name=cat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ranga U., Nagendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
RA Shankar S.K.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY064237; AAL51175.1; -; Genomic_DNA.
DR HSSP; P12506; 1TBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 72
SQ SEQUENCE 72 AA; 8385 MW; 656790CF4999FE3B CRC64;

Query Match 72.9%; Score 78; DB 2; Length 72;
Best Local Similarity 70.0%; Pred. No. 0.00088;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPASADGHR 20
DB 47 YGRKKRRQRRAPQSSSDHQ 66

RESULT 13
QBUMM6_9HIV1 PRELIMINARY; PRT; 72 AA.
AC QBUMM6;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Tat protein (Fragment).
GN Name=cat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ranga U., Nagendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
RA Shankar S.K.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY064236; AAL51174.1; -; Genomic_DNA.
DR HSSP; P12506; 1TBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
DR Activator; Nuclear protein; RNA-binding; Transcription;
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 72
SQ SEQUENCE 72 AA; 8385 MW; 656790CF4999FE3B CRC64;

Query Match 72.9%; Score 78; DB 2; Length 72;
Best Local Similarity 70.0%; Pred. No. 0.00088;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPASADGHR 20
DB 47 YGRKKRRQRRAPQSSSDHQ 66

RESULT 14
QBUMM7_9HIV1 PRELIMINARY; PRT; 72 AA.
AC QBUMM7;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
```

```
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 72
SQ SEQUENCE 72 AA; 8385 MW; 656790CF4999FE3B CRC64;

Query Match 72.9%; Score 78; DB 2; Length 72;
Best Local Similarity 70.0%; Pred. No. 0.00088;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPASADGHR 20
DB 47 YGRKKRRQRRAPQSSSDHQ 66

RESULT 13
QBUMM6_9HIV1 PRELIMINARY; PRT; 72 AA.
AC QBUMM6;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Tat protein (Fragment).
GN Name=cat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ranga U., Nagendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
RA Shankar S.K.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY064236; AAL51174.1; -; Genomic_DNA.
DR HSSP; P12506; 1TBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 72
SQ SEQUENCE 72 AA; 8385 MW; 656790CF4999FE3B CRC64;

Query Match 72.9%; Score 78; DB 2; Length 72;
Best Local Similarity 70.0%; Pred. No. 0.00088;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPASADGHR 20
DB 47 YGRKKRRQRRAPQSSSDHQ 66

RESULT 14
QBUMM7_9HIV1 PRELIMINARY; PRT; 72 AA.
AC QBUMM7;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
```

```

DR 07-FEB-2006, entry version 16.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
ON Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RA Ranga U., Narendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
RA Shankar S.K.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY064235; AAL51173.1; -; Genomic_DNA.
DR HSSP; P12506; 1TBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 72
SQ SEQUENCE 72 AA; 8428 MW; 13BCE610D7E0062B CRC64;

Query Match 72.9%; Score 78; DB 2; Length 72;
Best Local Similarity 70.0%; Pred. No. 0.00088;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRKPASADGHR 20
   |||||
DB 47 YGRKKRRQRRRAPQSSSDHQ 66
   |||||

RESULT 15
Q8UMM8_9HIV1 PRELIMINARY; PRT; 72 AA.
AC Q8UMM8;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Tat protein (Fragment).
DE Name=tat;
OS Human immunodeficiency virus 1.
ON Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RA Ranga U., Narendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
RA Shankar S.K.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY064234; AAL51172.1; -; Genomic_DNA.
DR HSSP; P12506; 1TBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat; 1.

DR PRINTS; PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON TER 72
SQ SEQUENCE 72 AA; 8385 MW; 656790CF4999FE3B CRC64;

Query Match 72.9%; Score 78; DB 2; Length 72;
Best Local Similarity 70.0%; Pred. No. 0.00088;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRKPASADGHR 20
   |||||
DB 47 YGRKKRRQRRRAPQSSSDHQ 66
   |||||

Search completed: August 24, 2006, 23:37:28
Job time : 302 secs
```



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:32:41 ; Search time 39 Seconds  
(without alignments)  
49.342 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 107

Sequence: 1 YGKKRRQRRKPASADGHR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	71.0	71	2 T09384	trans-activating t
2	71	66.4	86	2 A25700	trans-activating t
3	71	66.4	86	2 S33982	trans-activating t
4	71	66.4	95	1 TNLJ12	trans-activating t
5	71	66.4	101	1 E44001	trans-activating t
6	71	66.4	101	2 T09446	tat protein - huma
7	70	65.4	87	2 T01665	tat protein - huma
8	67	62.6	86	1 TNLJND	trans-activating t
9	64	59.8	72	1 TNLJH4	trans-activating t
10	62	57.9	86	1 TNLJZR	trans-activating t
11	62	57.9	86	2 JC5591	transactivator pro
12	62	57.9	86	2 S54381	tat protein - huma
13	53	49.5	953	2 B70681	probable xne prote
14	50	46.7	371	2 B39625	T-cell receptor al
15	50	46.7	399	2 A39625	T-cell receptor al
16	50	46.7	421	2 C96806	unknown protein t5
17	50	46.7	541	1 A43610	protein-tyrosine k
18	50	46.7	542	1 TVHUSC	protein-tyrosine k
19	49	45.8	37	2 T29829	protamine 23 - sma
20	49	45.8	367	2 S59329	probable membrane
21	48	44.9	269	2 B38095	T-cell-specific tr
22	48	44.9	272	2 A38900	T-cell-specific tr
23	48	44.9	303	2 JH0401	T-cell-specific tr
24	48	44.9	351	2 T23851	hypothetical prote
25	48	44.9	453	2 D81870	probable polynucle
26	48	44.9	453	2 H81151	polyA polymerase N
27	48	44.9	454	2 E64816	probable ATP-depen
28	48	44.9	455	2 D85388	probable ATP-depen
29	48	44.9	455	2 C90738	probable ATP-depen

30	47.5	44.4	100	1 TNLJSI	trans-activating t
31	47	43.9	88	2 A82800	hypothetical prote
32	47	43.9	90	2 B32986	variant surface gl
33	47	43.9	562	2 T49788	related to merozo
34	47	43.9	747	1 A57107	kinesin-related pr
35	47	43.9	770	2 G88445	protein C26E6.2 [i
36	47	43.9	1091	2 T13170	diaphanous protein
37	47	43.9	1196	2 T09356	brassinosteroid-in
38	46	43.0	41	2 A58213	green
39	46	43.0	397	2 A39565	lymphoid enhancer-
40	46	43.0	463	2 S37972	protamine - hum
41	46	43.0	501	2 I39360	low-temperature vi
42	46	43.0	819	2 T22152	IEF SSP 9502 - hum
43	46	43.0	2044	2 T13704	hypothetical prote
44	45	42.1	91	2 A59493	still life protein
45	45	42.1	128	2 H70457	protamine P2 - Sty
					ribosomal protein

ALIGNMENTS

RESULT 1

T09384

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate t  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 31-Dec-2004  
C;Accession: T09384

R;Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Bir  
J. Virol. 69, 4228-4236, 1995  
A;Title: Defective accessory genes in a human immunodeficiency virus type 1-infected long  
A;Reference number: 216654; MUID:95287475; PMID:7769682

A;Accession: T09384

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-71 <MIC>

A;Cross-references: UNIPROT:Q71926; UNIPARC:UPI00000FF00C; EMBL:U24451; NID:9829440; PID  
C;Genetics:  
C;Gene: tat

C;Superfamily: leukemia virus trans-activating transcription regulator

C;Keywords: transcription

Query Match 71.0%; Score 76; DB 2; Length 71;  
Best Local Similarity 65.0%; Pred. No. 0.0014;  
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGKKRRQRRKPASADGHR 20

|||||

Db 47 YGKKRRQRRRPQDSEAHQ 66

RESULT 2

A25700

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate t  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 28-Sep-1987 #sequence\_revision 28-Sep-1987 #text\_change 31-Dec-2004  
C;Accession: A25700

R;Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, F.; Haseltine, W.

Science 229, 74-77, 1985

A;Reference number: A25700; MUID:85244627; PMID:2390041

A;Accession: A25700

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-86 <SOD>

A;Cross-references: UNIPROT:P04610; UNIPARC:UPI000011F40

C;Superfamily: leukemia virus trans-activating transcription regulator

Query Match 66.4%; Score 71; DB 2; Length 86;  
Best Local Similarity 65.0%; Pred. No. 0.0075;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKKRRQRRKPASADGHR 20

|||||

Db 47 YGKKRRQRRRPQGSQTHQ 66

RESULT 3  
S33982  
trans-activating transcription regulator - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 06-Oct-1994 #sequence\_revision 23-Feb-1996 #text\_change 31-Dec-2004  
C/Accession: S33982; S26385; S19864  
R;Carlini, F.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33982  
A:Molecule type: DNA  
A:Residues: 1-86 <CAR>  
A:Cross-references: UNIPROT:P04606; UNIPARC:UPI0000000419; EMBL:Z11530; NID:G60192; PIDN:R;Siderovski, D.P.; Matsuyama, T.; Frigerio, E.; Chui, S.; Min, X.; Erfle, H.; Summer-Sh Nucleic Acids Res. 20, 5311-5320, 1992  
A:Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activator A:Reference number: S26385; MUID:93065196; PMID:1437550  
A:Accession: S26385  
A:Molecule type: nucleic acid  
A:Residues: 1-86 <SID>  
A:Cross-references: UNIPARC:UPI0000000419; EMBL:X64650; NID:G60144; PIDN:CAA45921.1; PIDN:CA:10-814-109-2.rpr  
C:Genetics:  
A:Gene: tat  
A:Introns: 72/2  
A:Superfamily: leukemia virus trans-activating transcription regulator  
C:Keywords: AIDS; immunodeficiency

Query Match 66.4%; Score 71; DB 2; Length 86;  
Best Local Similarity 65.0%; Pred. No. 0.0075;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRKPASADGHR 20  
||||||| : :  
Db 47 YGRKKRRQRRRPPQGSQTHQ 66

RESULT 4  
TNLJ12  
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C>Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 31-Dec-2004  
C/Accession: A04017  
R;Arya, S.K.; Gallo, R.C.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986  
A:Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity of A:Reference number: A94093; MUID:86177573; PMID:3008154  
A:Accession: A04017  
A:Molecule type: DNA  
A:Residues: 1-95 <ARY>  
A:Cross-references: UNIPROT:P04326; UNIPARC:UPI0000174A54  
C:Genetics:  
A:Gene: tat  
A:Superfamily: leukemia virus trans-activating transcription regulator  
C:Keywords: AIDS; immunodeficiency

Query Match 66.4%; Score 71; DB 1; Length 95;  
Best Local Similarity 65.0%; Pred. No. 0.0082;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRKPASADGHR 20  
||||||| : :  
Db 56 YGRKKRRQRRRAPQGSQTHQ 75

RESULT 5  
E44001  
trans-activating transcription regulator - human immunodeficiency virus type 1 (strain N;Alternate names: tat protein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)

C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Dec-2004  
C/Accession: E44001  
R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.  
J. Virol. 66, 6587-6600, 1992  
A:Title: Complete nucleotide sequence, genome organization, and biological properties of A:Reference number: A44001; MUID:93021387; PMID:1404605  
A:Accession: E44001  
A:Molecule type: DNA  
A:Residues: 1-101 <LIY>  
A:Cross-references: UNIPROT:P35965; UNIPARC:UPI0000136937; GB:M93258  
C:Genetics:  
A:Gene: tat  
A:Introns: 72/2  
A:Superfamily: leukemia virus trans-activating transcription regulator  
C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 66.4%; Score 71; DB 1; Length 101;  
Best Local Similarity 65.0%; Pred. No. 0.0086;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRKPASADGHR 20  
||||||| : :  
Db 47 YGRKKRRQRRRPPQDSQTHQ 66

RESULT 6  
T09446  
tat protein - human immunodeficiency virus type 1 (strain JRFL)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 31-Dec-2004  
C/Accession: T09446  
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996  
A:Reference number: Z16673  
A:Accession: T09446  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-101 <PAN>  
A:Cross-references: UNIPROT:Q75758; UNIPARC:UPI0000109776; EMBL:U63632; NID:G1465777; PIDN:CA:10-814-109-2.rpr  
C:Genetics:  
A:Gene: tat  
A:Introns: 72/2  
A:Superfamily: leukemia virus trans-activating transcription regulator

Query Match 66.4%; Score 71; DB 2; Length 101;  
Best Local Similarity 65.0%; Pred. No. 0.0086;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRKPASADGHR 20  
||||||| : :  
Db 47 YGRKKRRQRRRAPQDSQTHQ 66

RESULT 7  
T01665  
tat protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 31-Dec-2004  
C/Accession: T01665  
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.  
Cell 46, 63-74, 1986  
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol. A:Reference number: Z14389; MUID:86245056; PMID:2424612  
A:Accession: T01665  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-87 <ALI>  
A:Cross-references: UNIPROT:P04613; UNIPARC:UPI00001132A9; EMBL:K03456; NID:G60228; PIDN:CA:10-814-109-2.rpr  
C:Genetics:  
A:Introns: 72/2  
A:Superfamily: leukemia virus trans-activating transcription regulator

Query Match 65.4%; Score 70; DB 2; Length 87;

Best Local Similarity 65.0%; Pred. No. 0.01;  
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPPASADGHR 20  
|||||  
Db 47 YGRKKRRQRRKPPQGNQAHQ 66

RESULT 8  
TNLJND  
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 31-Dec-2004  
R;Spire, B.; Sire, J.; Zachar, V.; Rey, P.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;  
Gene 81, 275-284, 1989  
A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunodeficiency virus  
A;Reference number: JQ0065; MUID:90034200; PMID:2806917  
A;Accession: JQ0071  
A;Molecule type: DNA  
A;Residues: 1-86 <SPI>  
A;Cross-references: UNIPROT:P18804; UNIPARC:UPI000011D5D6; GB:M27323; NID:g328154; PIDN:  
C;Genetics: tat  
C;Superfamily: leukemia virus trans-activating transcription regulator  
C;Keywords: AIDS; immunodeficiency; transcription

Query Match 62.6%; Score 67; DB 1; Length 86;  
Best Local Similarity 60.0%; Pred. No. 0.026; Indels 0; Gaps 0;  
Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPPASADGHR 20  
|||||  
Db 47 YGRKKRRQRRKPPQGDQAHQ 66

RESULT 9  
TNLJH4  
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 31-Dec-2004  
R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, R.;  
Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986  
A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human  
A;Reference number: A94136; MUID:87041461; PMID:3490666  
A;Accession: B25523  
A;Molecule type: DNA  
A;Residues: 1-72 <DES>  
A;Cross-references: UNIPARC:UPI0000174A55; GB:M13137; NID:g326460  
A;Note: the GenBank entry ADRE3AA PID:g209908 differs from the published sequence in tra  
C;Genetics: tat  
C;Superfamily: leukemia virus trans-activating transcription regulator  
C;Keywords: transcription regulation

Query Match 59.8%; Score 64; DB 1; Length 72;  
Best Local Similarity 60.0%; Pred. No. 0.057; Indels 0; Gaps 0;  
Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPPASADGHR 20  
|||||  
Db 47 YGRKKRRQRRRAHQDSQNHQ 66

RESULT 10  
TNLJZR  
trans-activating transcription regulator - human immunodeficiency virus Zr-6  
C;Species: human immunodeficiency virus Zr-6  
C;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 31-Dec-2004  
R;Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu

Gene 52, 71-82, 1987  
A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotide  
A;Reference number: A26192; MUID:87248097; PMID:3036660  
A;Accession: C26192  
A;Molecule type: DNA  
A;Residues: 1-86 <SPI>  
A;Cross-references: UNIPROT:P04609; UNIPARC:UPI000013693A; GB:K03458; GB:M16322; NID:g32  
C;Genetics: tat  
A;Gene: tat  
A;Introns: 72/3  
C;Superfamily: leukemia virus trans-activating transcription regulator  
C;Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 57.9%; Score 62; DB 1; Length 86;  
Best Local Similarity 60.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPPASADGHR 20  
|||||  
Db 47 YGRKKRRQRRRPSQGGQTHQ 66

RESULT 11  
JCS591  
transactivator protein - human immunodeficiency virus type 1  
N;Alternate names: tat protein  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 31-Dec-2004  
C;Accession: JCS591  
R;Hoffmann, S.; Willbold, D.  
Biochem. Biophys. Res. Commun. 235, 806-811, 1997  
A;Title: A selection system to study protein-RNA interactions: Functional display of HIV  
A;Reference number: JCS591; MUID:97350867; PMID:9207243  
A;Accession: JCS591  
A;Molecule type: protein  
A;Residues: 1-86 <HO2>  
A;Cross-references: UNIPARC:UPI000017865E  
C;Comment: This protein is a key regulatory protein in the viral replication cycle and be  
C;Superfamily: leukemia virus trans-activating transcription regulator  
F;22-31/Region: cysteine-rich

Query Match 57.9%; Score 62; DB 2; Length 86;  
Best Local Similarity 60.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPPASADGHR 20  
|||||  
Db 47 YGRKKRRQRRRPSQGGQTHQ 66

RESULT 12  
S54381  
tat protein - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 31-Dec-2004  
C;Accession: S54381  
R;Theodore, T.; Buckler-White, A.J.  
submitted to the EMBL Data Library, July 1989  
A;Reference number: S54377  
A;Accession: S54381  
A;Status: preliminary  
A;Molecule type: genomic RNA  
A;Residues: 1-86 <THE>  
A;Cross-references: UNIPROT:P12506; UNIPARC:UPI0000136938; EMBL:M22639; NID:g329377; PID  
C;Genetics: 72/2  
C;Superfamily: leukemia virus trans-activating transcription regulator

Query Match 57.9%; Score 62; DB 2; Length 86;  
Best Local Similarity 60.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPPASADGHR 20

A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-399 <WAT>  
 A;Cross-references: UNIPROT:Q9UJU2; UNIPARC:UPI0000052242  
 C;Keywords: T-cell receptor  
 F;296-371/Domain: HMG box homology <HMG1>

Query Match 46.7%; Score 50; DB 2; Length 399;  
 Best Local Similarity 50.0%; Pred. No. 17;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGKKRRQRRRKPASADG 18  
 ||:||||:|:|  
 Db 372 YGKKRRKREKLOESASG 389

Search completed: August 24, 2006, 23:38:13  
 Job time : 42 secs

Db 47 YGKKRRQRRRPSQGQTHQ 66  
 |||||  
 RESULT 13  
 B70681  
 probable rne protein - Mycobacterium tuberculosis (strain H37RV)  
 C;Species: Mycobacterium tuberculosis  
 C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
 C;Accession: B70681  
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, K.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A;Reference number: A70500; MUID:98295987; PMID:9634230  
 A;Accession: B70681  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-953 <COL>  
 A;Cross-references: UNIPROT:P71905; UNIPARC:UPI000000D5011; GB:Z81451; GB:AL123456; NID:9  
 A;Experimental source: strain H37RV  
 C;Genetics:  
 A;Gene: rne

Query Match 49.5%; Score 53; DB 2; Length 953;  
 Best Local Similarity 66.7%; Pred. No. 14;  
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RKRRQRRRKPASAD 17  
 ||:|||||  
 Db 230 RRRRRRRKKSASGD 244

RESULT 14  
 B39625  
 T-cell receptor alpha enhancer-binding protein, short form - human  
 C;Species: Homo sapiens (man)  
 C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 31-Dec-2004  
 C;Accession: B39625  
 R;Waterman, M.L.; Fischer, W.H.; Jones, K.A. Genes Dev. 5, 656-669, 1991  
 A;Title: A thymus-specific member of the HMG protein family regulates the human T cell  
 A;Reference number: A39625; MUID:91184620; PMID:2010090  
 A;Accession: B39625  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-371 <WAT>  
 A;Cross-references: UNIPARC:UPI000017A223  
 C;Keywords: T-cell receptor  
 F;288-343/Domain: HMG box homology <HMG1>

Query Match 46.7%; Score 50; DB 2; Length 371;  
 Best Local Similarity 50.0%; Pred. No. 16;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGKKRRQRRRKPASADG 18  
 ||:||||:|:|  
 Db 344 YGKKRRKREKLOESASG 361

RESULT 15  
 A39625  
 T-cell receptor alpha enhancer-binding protein, long form - human  
 C;Species: Homo sapiens (man)  
 C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 31-Dec-2004  
 C;Accession: A39625  
 R;Waterman, M.L.; Fischer, W.H.; Jones, K.A. Genes Dev. 5, 656-669, 1991  
 A;Title: A thymus-specific member of the HMG protein family regulates the human T cell  
 A;Reference number: A39625; MUID:91184620; PMID:2010090  
 A;Accession: A39625

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:39:22 ; Search time 32 Seconds  
(without alignments)  
42.764 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 107

Sequence: 1 YGRKKRQRRRKPASADGHR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	66.4	20	6	US-10-539-677-37
2	71	66.4	36	7	US-11-286-920-6
3	71	66.4	229	6	US-10-533-841-54
4	71	66.4	293	6	US-10-533-841-52
5	71	66.4	715	6	US-10-533-841-60
6	71	66.4	779	6	US-10-533-841-58
7	71	66.4	1078	6	US-10-533-841-67
8	71	66.4	1141	6	US-10-533-841-71
9	71	66.4	1141	6	US-10-533-841-79
10	71	66.4	1141	6	US-10-533-841-81
11	71	66.4	1141	6	US-10-533-841-83
12	71	66.4	1142	6	US-10-533-841-69
13	71	66.4	1142	6	US-10-533-841-73
14	71	66.4	1142	6	US-10-533-841-75
15	71	66.4	1142	6	US-10-533-841-77
16	70	65.4	20	6	US-10-539-677-36
17	70	65.4	29	7	US-11-251-734-4
18	65	60.7	20	6	US-10-539-677-38
19	64	59.8	14	7	US-11-142-051-4
20	62	57.9	20	6	US-10-539-677-34
21	62	57.9	34	7	US-11-223-610-46
22	61	57.0	20	6	US-10-539-677-35
23	58	54.2	11	6	US-10-547-530-78
24	58	54.2	11	6	US-10-518-710-4
25	58	54.2	11	6	US-10-559-806A-1

26	58	54.2	11	7	US-11-318-535-24	Sequence 24, Appl
27	58	54.2	11	7	US-11-223-610-45	Sequence 45, Appl
28	58	54.2	11	7	US-11-267-986-8	Sequence 8, Appl
29	58	54.2	11	7	US-11-267-817-19	Sequence 19, Appl
30	58	54.2	11	7	US-11-271-285-59	Sequence 59, Appl
31	58	54.2	11	7	US-11-317-806-85	Sequence 85, Appl
32	58	54.2	11	7	US-11-238-035-39	Sequence 39, Appl
33	58	54.2	11	7	US-11-250-830-1	Sequence 1, Appl
34	58	54.2	11	7	US-11-241-836-16	Sequence 16, Appl
35	58	54.2	12	7	US-11-264-074-19	Sequence 19, Appl
36	58	54.2	14	7	US-11-318-535-7	Sequence 7, Appl
37	58	54.2	14	7	US-11-318-535-8	Sequence 8, Appl
38	58	54.2	15	6	US-10-539-677-13	Sequence 13, Appl
39	58	54.2	15	7	US-11-267-986-7	Sequence 7, Appl
40	58	54.2	15	7	US-11-238-035-40	Sequence 40, Appl
41	58	54.2	15	7	US-11-250-830-19	Sequence 19, Appl
42	58	54.2	15	7	US-11-241-836-17	Sequence 17, Appl
43	58	54.2	23	7	US-11-240-962-1	Sequence 1, Appl
44	58	54.2	36	7	US-11-251-643-23	Sequence 23, Appl
45	58	54.2	36	7	US-11-251-643-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-10-539-677-37  
; Sequence 37, Application US/10539677  
; Publication No. US20060104988A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Maryland Biotechnology Institute  
; APPLICANT: Fauza, C. David  
; APPLICANT: Tikhonov, Ilia  
; TITLE OF INVENTION: VACCINES AGAINST HIV-1 PROTEIN TO GENERATE NEUTRALIZING  
; TITLE OF INVENTION: ANTIBODIES  
; FILE REFERENCE: 4115-194  
; CURRENT APPLICATION NUMBER: US/10/539,677  
; CURRENT FILING DATE: 2005-06-16  
; PRIOR APPLICATION NUMBER: US 60/434,368  
; PRIOR FILING DATE: 2002-12-18  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 37  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
US-10-539-677-37

Query Match 66.4%; Score 71; DB 6; Length 20;  
Best Local Similarity 68.4%; Pred. No. 0.002;  
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 YGRKKRQRRRKPASADGH 19  
||| ||||| ||| : :  
Db 2 YGRKKRQRRSAPSSSEDH 20

RESULT 2  
US-11-286-920-6  
; Sequence 6, Application US/11286920  
; Publication No. US20060166881A1  
; GENERAL INFORMATION:  
; APPLICANT: Washington University  
; APPLICANT: Hotchkiss, Richard  
; APPLICANT: Fivnica-Worms, David  
; APPLICANT: McDunn, Jonathan  
; TITLE OF INVENTION: Membrane-Permeant Peptide Complexes for Treatment of Sepsis  
; FILE REFERENCE: 60005161-0204  
; CURRENT APPLICATION NUMBER: US/11/286,920  
; CURRENT FILING DATE: 2005-11-23  
; PRIOR APPLICATION NUMBER: US 10/374,035

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; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 10/368,280
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 09/557,465
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/336,093
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: US 60/090,087
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-286-920-6

Query Match          66.4%; Score 71; DB 7; Length 36;
Best Local Similarity 65.0%; Pred. No. 0.0034;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKKRRQRRRKPPASADGHR 20
Db 11 YGKKRRQRRRKPPQGSQTHQ 30

RESULT 3
US-10-533-841-54
; Sequence 54, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 trNef-Tatm fusion
US-10-533-841-54

Query Match          66.4%; Score 71; DB 6; Length 229;
Best Local Similarity 65.0%; Pred. No. 0.018;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKKRRQRRRKPPASADGHR 20
Db 190 YGKKRRQRRRKPPQGSQTHQ 209

RESULT 4
US-10-533-841-52
; Sequence 52, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05

; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 Nef-Tatm fusion
US-10-533-841-52

Query Match          66.4%; Score 71; DB 6; Length 293;
Best Local Similarity 65.0%; Pred. No. 0.023;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKKRRQRRRKPPASADGHR 20
Db 254 YGKKRRQRRRKPPQGSQTHQ 273

RESULT 5
US-10-533-841-60
; Sequence 60, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c Nef-Tatm fusion
US-10-533-841-60

Query Match          66.4%; Score 71; DB 6; Length 715;
Best Local Similarity 65.0%; Pred. No. 0.05;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKKRRQRRRKPPASADGHR 20
Db 676 YGKKRRQRRRKPPQGSQTHQ 695

RESULT 6
US-10-533-841-58
; Sequence 58, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: HIV-1 ds-gp120c'
US-10-533-841-58

Query Match          66.4%; Score 71; DB 6; Length 779;
Best Local Similarity 65.0%; Pred. No. 0.054;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKRRRRRRKPPASADGHR 20
Db 740 YGKRRRRRRPPQGSQTHQ 759

RESULT 7
US-10-533-841-67
; Sequence 67, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 1078
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 trNef Tatm fusion
US-10-533-841-67

Query Match          66.4%; Score 71; DB 6; Length 1078;
Best Local Similarity 65.0%; Pred. No. 0.073;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKRRRRRRKPPASADGHR 20
Db 1039 YGKRRRRRRPPQGSQTHQ 1058

RESULT 8
US-10-533-841-71
; Sequence 71, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 mNef Tatm fusion
US-10-533-841-71

Query Match          66.4%; Score 71; DB 6; Length 1141;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 mNef Tatm fusion
US-10-533-841-71

Query Match          66.4%; Score 71; DB 6; Length 1141;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKRRRRRRKPPASADGHR 20
Db 1102 YGKRRRRRRPPQGSQTHQ 1121

RESULT 9
US-10-533-841-79
; Sequence 79, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 1141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 mLL-Nef Tatm fusion
US-10-533-841-79

Query Match          66.4%; Score 71; DB 6; Length 1141;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKRRRRRRKPPASADGHR 20
Db 1102 YGKRRRRRRPPQGSQTHQ 1121

RESULT 10
US-10-533-841-81
; Sequence 81, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 1141
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 mLL-Nef Tatm fusion
US-10-533-841-81

Query Match          66.4%; Score 71; DB 6; Length 1141;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKRRRRRRKPPASADGHR 20
Db 1102 YGKRRRRRRPPQGSQTHQ 1121

RESULT 11
US-10-533-841-83
```

```
; Sequence 83, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 mL2-Nef Tatm fusion
US-10-533-841-83

Query Match          66.4%; Score 71; DB 6; Length 1141;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRKPPASADGHR 20
Db 1102 YGRKKRRQRRRPQGSQTHQ 1121

RESULT 12
US-10-533-841-69
; Sequence 69, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 Nef Tatm fusion
US-10-533-841-69

Query Match          66.4%; Score 71; DB 6; Length 1142;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRKPPASADGHR 20
Db 1103 YGRKKRRQRRRPQGSQTHQ 1122

RESULT 13
US-10-533-841-73
; Sequence 73, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
```

```
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 L1-Nef Tatm fusion
US-10-533-841-73

Query Match          66.4%; Score 71; DB 6; Length 1142;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRKPPASADGHR 20
Db 1103 YGRKKRRQRRRPQGSQTHQ 1122

RESULT 14
US-10-533-841-75
; Sequence 75, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 L2-Nef Tatm fusion
US-10-533-841-75

Query Match          66.4%; Score 71; DB 6; Length 1142;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRRKPPASADGHR 20
Db 1103 YGRKKRRQRRRPQGSQTHQ 1122

RESULT 15
US-10-533-841-77
; Sequence 77, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
; APPLICANT: ERTL, Peter F.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: PG5023
; CURRENT APPLICATION NUMBER: US/10/533,841
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: PCT/EP 03/12402
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: GB 0225788.9
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
```



```
; SEQ ID NO 77
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 LL-Nef Tatm fusion
US-10-533-841-77

Query Match      66.4%; Score 71; DB 6; Length 1142;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 YGRKRRQRRRKPSADGHR 20
      |||||
Db      1103 YGRKRRQRRRPQGSQTHQ 1122
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Search completed: August 24, 2006, 23:42:57  
Job time : 33 secs

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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:38:27 ; Search time 185 Seconds  
(without alignments)  
50.077 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 107

Sequence: 1 YGRKKRRQRRKPASADGHR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SID33/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	20	5	US-10-814-109-2
2	79	73.8	101	4	US-10-190-435-211
3	78	72.9	101	4	US-10-190-435-221
4	78	72.9	101	5	US-10-780-507-110
5	75	70.1	101	4	US-10-190-435-227
6	75	70.1	101	6	US-11-205-883A-6
7	75	70.1	1896	4	US-10-296-734-393
8	75	70.1	5747	4	US-10-296-734-405
9	74	69.2	101	4	US-10-190-435-213
10	74	69.2	101	5	US-10-501-223-1
11	74	69.2	101	5	US-10-501-223-20
12	74	69.2	101	5	US-10-501-223-21
13	74	69.2	101	5	US-10-501-223-22
14	74	69.2	101	5	US-10-501-223-41
15	74	69.2	101	5	US-10-501-223-42
16	74	69.2	101	5	US-10-501-223-43
17	74	69.2	101	5	US-10-501-223-74
18	73	68.2	101	6	US-11-135-597-219
19	73	68.2	102	4	US-10-770-668-50
20	73	68.2	1893	4	US-10-296-734-399
21	72	67.3	99	4	US-10-190-435-215
22	72	67.3	99	4	US-10-190-435-218
23	72	67.3	100	5	US-10-969-191-16
24	72	67.3	101	4	US-10-190-435-208
25	72	67.3	101	4	US-10-190-435-210
26	72	67.3	101	4	US-10-190-435-212
27	72	67.3	101	4	US-10-190-435-216

```

28 72 67.3 101 4 US-10-190-435-217 Sequence 217, App
29 72 67.3 101 4 US-10-190-435-219 Sequence 219, App
30 72 67.3 101 4 US-10-190-435-220 Sequence 220, App
31 72 67.3 101 4 US-10-190-435-222 Sequence 222, App
32 72 67.3 101 4 US-10-190-435-223 Sequence 223, App
33 72 67.3 101 4 US-10-190-435-224 Sequence 224, App
34 72 67.3 101 4 US-10-190-435-225 Sequence 225, App
35 72 67.3 101 4 US-10-190-435-226 Sequence 226, App
36 72 67.3 101 4 US-10-387-336-86 Sequence 86, Appl
37 72 67.3 101 5 US-10-799-854-50 Sequence 50, Appl
38 72 67.3 101 5 US-10-799-854-63 Sequence 63, Appl
39 72 67.3 101 5 US-10-780-507-111 Sequence 111, App
40 72 67.3 101 5 US-10-494-131-2 Sequence 2, Appli
41 72 67.3 101 5 US-10-494-131-4 Sequence 4, Appli
42 72 67.3 101 5 US-10-494-131-18 Sequence 18, Appli
43 72 67.3 101 6 US-11-135-597-223 Sequence 223, App
44 72 67.3 101 6 US-11-135-597-224 Sequence 224, App
45 72 67.3 101 6 US-11-135-597-226 Sequence 226, App

```

#### ALIGNMENTS

##### RESULT 1

```

US-10-814-109-2
; Sequence 2, Application US/10814109
; Publication No. US20050222042A1
; GENERAL INFORMATION:
; APPLICANT: Salter, Michael
; APPLICANT: Gingrich, Jeffrey
; TITLE OF INVENTION: Method for Modification of NMDA Receptors Through Inhibition of S
; FILE REFERENCE: 2560.004
; CURRENT APPLICATION NUMBER: US/10/814,109
; CURRENT FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-814-109-2

```

```

Query Match 100.0%; Score 107; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 YGRKKRRQRRKPASADGHR 20
Db 1 YGRKKRRQRRKPASADGHR 20

```

##### RESULT 2

```

US-10-190-435-211
; Sequence 211, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

; OTHER INFORMATION: Description of Artificial Sequence: Tat TV006  
US-10-190-435-211

Query Match 73.8%; Score 79; DB 4; Length 101;  
Best Local Similarity 70.0%; Pred. No. 0.0019;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKRRRQRRRKPPASADGHR 20  
|||  
Db 47 YGRKRRRQRRRSTPPSSEGHQ 66  
|||

### RESULT 3

```

US-10-190-435-221
; Sequence 221, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYPEPTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: P818133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 101

```

; TYPE: PRT

**ORGANISM: Artificial Sequence**

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Tat 301904-Ind

## US-10-190-435-221

```

Query Match          72.9%; Score 78; DB 4; Length 101;
Best Local Similarity 70.0%; Pred. NO. 0.0026;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

Qy 1 YGRKRRQRRRRKPASADGHR 20  
|||  
Dy 47 YGRKRRQRRRRAPQSSDHD 66  
|||

## DEC 11 1964

```

US-10-780-507-110
; Sequence 110, Application US/10780507
; Publication No. US20050137387A1
; GENERAL INFORMATION:
; APPLICANT: MULLINS, James I.
; APPLICANT: RODRIGO, Allen G.
; APPLICANT: LEARN, Gerald H.
; APPLICANT: Li, Fusheng
; APPLICANT: NICKLE, David C.
; APPLICANT: JENSEN, Mark A.
; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOUNDS
; FILE REFERENCE: 16336-001320US
; CURRENT APPLICATION NUMBER: US/10/780,507
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 10/204,204
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US01/05288
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 60/183,659
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US 60/447,586
; PRIOR FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
; LENGTH: 101

```

```

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Most recent common ancestor reconstructions of clade C tat protein
; OTHER INFORMATION: n sequence
US-10-780-507-110

```

Query Match 72.9%; Score 78; DB 5; Length 101;  
Best Local Similarity 70.0%; Pred. No. 0.0026;  
Matches 14; Conservative 3; Mismatches 3; Indels

Qy 1 YGKKRRQRRRKPASADGHR 20  
|||  
Db 47 YGKKRRQRRRAPPSSEDDHQ 66  
|||

RESULT 5

```

RESUL1 5
US-10-190-435-227
; Sequence 227, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190.435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 227
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tat C2220-Ech
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (40)
; OTHER INFORMATION: where Xaa = unknown amino acid
; US-10-190-435-227

```

Query Match 70.1%; Score 75; DB 4; Length 101;  
Best Local Similarity 70.0%; Pred. No. 0.007;  
Matches 14: Conservative 2; Mismatches 4; Indels

Qy 1 YGRKKRRQRRRKPASADGHR 20  
|||  
47 YGRKKRRQRRRAPQSSKPDHO 66  
pb

PROFIT E

```

RESUL1 6
US-11-205-883A-6
; Sequence 6, Application US/11205883A
; Publication No. US2006069469A1
; GENERAL INFORMATION:
; APPLICANT: PAYNE, SHELLEY M.
; APPLICANT: DUDLEY, JACQUELIN P.
; APPLICANT: SELIGER, STEFAN S.
; APPLICANT: FENG, ZHENGYU
; TITLE OF INVENTION: BACTERIAL VECTOR SYSTEMS
; FILE REFERENCE: CULFR.0301US
; CURRENT APPLICATION NUMBER: US/11/205,883A
; CURRENT FILING DATE: 2005-08-17
; PRIOR APPLICATION NUMBER: 60/602,276
; PRIOR FILING DATE: 2004-08-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 101

```

Qy 1 YGRKKRRQRRRKPASADGHR 20  
|||  
Db 47 YGRKKRRQRRRSPQDSETHQ 66  
|||

RESULT 11  
US-10-501-223-20  
; Sequence 20, Application US/10501223  
; Publication No. US20050164164A1  
; GENERAL INFORMATION:  
; APPLICANT: GUILLON, CHRISTOPHE  
; APPLICANT: CHEDAL-BORNU, AURELIE  
; APPLICANT: VERRIER, BERNARD  
; APPLICANT: MANDRAND, BERNARD  
; TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS  
; FILE REFERENCE: 0508-1107  
; CURRENT APPLICATION NUMBER: US/10/501.223  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: PCT/FR03/00051  
; PRIOR FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: FR 02/00319  
; PRIOR FILING DATE: 2002-01-11  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: G79A-K89L  
; OTHER INFORMATION: mutant of Tat protein  
US-10-501-223-20

Query Match 69.2%; Score 74; DB 5; Length 101;  
Best Local Similarity 65.0%; Pred. No. 0.0096;  
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRKPSADGHR 20  
||||||| : : :  
DB 47 YGRKKRRQRRSPQDSETHQ 66

RESULT 12  
US-10-501-223-21  
; Sequence 21, Application US/10501223  
; Publication No. US20050164164A1  
; GENERAL INFORMATION:  
; APPLICANT: GUILLON, CHRISTOPHE  
; APPLICANT: CHEDAL-BORNU, AURELIE  
; APPLICANT: VERRIER, BERNARD  
; APPLICANT: MANDRAND, BERNARD  
; TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS  
; FILE REFERENCE: 0508-1107  
; CURRENT APPLICATION NUMBER: US/10/501.223  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: PCT/FR03/00051  
; PRIOR FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: FR 02/00319  
; PRIOR FILING DATE: 2002-01-11  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 21  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: G79A-E92Q  
; OTHER INFORMATION: mutant of Tat protein  
US-10-501-223-21

Query Match 69.2%; Score 74; DB 5; Length 101;  
Best Local Similarity 65.0%; Pred. No. 0.0096;  
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRKPSADGHR 20  
||||||| : : :  
DB 47 YGRKKRRQRRSPQDSETHQ 66

Db 47 YGRKKRRQRRSPQDSETHQ 66

RESULT 13  
US-10-501-223-22  
; Sequence 22, Application US/10501223  
; Publication No. US20050164164A1  
; GENERAL INFORMATION:  
; APPLICANT: GUILLON, CHRISTOPHE  
; APPLICANT: CHEDAL-BORNU, AURELIE  
; APPLICANT: VERRIER, BERNARD  
; APPLICANT: MANDRAND, BERNARD  
; TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS  
; FILE REFERENCE: 0508-1107  
; CURRENT APPLICATION NUMBER: US/10/501.223  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: PCT/FR03/00051  
; PRIOR FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: FR 02/00319  
; PRIOR FILING DATE: 2002-01-11  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 22  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: K89L-E92Q  
; OTHER INFORMATION: mutant of Tat protein  
US-10-501-223-22

Query Match 69.2%; Score 74; DB 5; Length 101;  
Best Local Similarity 65.0%; Pred. No. 0.0096;  
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRKPSADGHR 20  
||||||| : : :  
DB 47 YGRKKRRQRRSPQDSETHQ 66

RESULT 14  
US-10-501-223-41  
; Sequence 41, Application US/10501223  
; Publication No. US20050164164A1  
; GENERAL INFORMATION:  
; APPLICANT: GUILLON, CHRISTOPHE  
; APPLICANT: CHEDAL-BORNU, AURELIE  
; APPLICANT: VERRIER, BERNARD  
; APPLICANT: MANDRAND, BERNARD  
; TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS  
; FILE REFERENCE: 0508-1107  
; CURRENT APPLICATION NUMBER: US/10/501.223  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: PCT/FR03/00051  
; PRIOR FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: FR 02/00319  
; PRIOR FILING DATE: 2002-01-11  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 41  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: C27S-G79A-K89L  
; OTHER INFORMATION: mutant of Tat protein  
US-10-501-223-41

Query Match 69.2%; Score 74; DB 5; Length 101;  
Best Local Similarity 65.0%; Pred. No. 0.0096;  
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRKPSADGHR 20

Db 47 YGRKKRQRRRSPQDSETHQ 66

RESULT 15  
US-10-501-223-42  
; Sequence 42, Application US/10501223  
; Publication No. US20050164164A1  
; GENERAL INFORMATION:  
; APPLICANT: GUILLOIN, CHRISTOPHE  
; APPLICANT: CHEDAL-BORNU, AURELIE  
; APPLICANT: VERRIER, BERNARD  
; APPLICANT: MANDRAND, BERNARD  
; TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS  
; FILE REFERENCE: 0508-1107  
; CURRENT APPLICATION NUMBER: US/10/501,223  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: PCT/FR03/00051  
; PRIOR FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: FR 02/00319  
; PRIOR FILING DATE: 2002-01-11  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 42  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: C27S-G79A-E92Q  
; OTHER INFORMATION: mutant of Tat protein  
US-10-501-223-42

Query Match 69.2%; Score 74; DB 5; Length 101;  
Best Local Similarity 65.0%; Pred. No. 0.0096;  
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRRKPASADGHR 20  
Db 47 YGRKKRQRRRSPQDSETHQ 66

Search completed: August 24, 2006, 23:42:19  
Job time : 186 secs

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Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2006, 23:37:42 ; Search time 50 Seconds  
(without alignments)  
35.012 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 107

Sequence: 1 YGRKRRRRRKPASADGHR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCUTUS\_COMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	73	68.2	101 2	US-10-290-579A-219
2	72	67.3	101 2	US-09-475-515-86
3	72	67.3	101 2	US-10-290-579A-223
4	72	67.3	101 2	US-10-290-579A-224
5	72	67.3	101 2	US-10-290-579A-226
6	72	67.3	102 2	US-09-475-515-90
7	71	66.4	26 1	US-08-450-257-48
8	71	66.4	26 1	US-08-450-246-48
9	71	66.4	26 1	US-08-450-098-48
10	71	66.4	26 1	US-08-451-233-48
11	71	66.4	26 1	US-08-450-236-48
12	71	66.4	26 1	US-08-235-403-48
13	71	66.4	35 1	US-08-450-257-49
14	71	66.4	35 1	US-08-450-246-49
15	71	66.4	35 1	US-08-450-098-49
16	71	66.4	35 1	US-08-451-233-49
17	71	66.4	35 1	US-08-450-236-49
18	71	66.4	35 2	US-08-235-403-49
19	71	66.4	36 1	US-08-450-257-2
20	71	66.4	36 1	US-08-450-246-2
21	71	66.4	36 1	US-08-450-098-2
22	71	66.4	36 1	US-08-451-233-2
23	71	66.4	36 1	US-08-450-236-2
24	71	66.4	36 2	US-09-113-921-55
25	71	66.4	36 2	US-08-235-403-2
26	71	66.4	36 2	US-09-336-093-6

27	71	66.4	36 2	US-09-409-624-1	Sequence 1, Appli
28	71	66.4	36 2	US-09-409-624-2	Sequence 2, Appli
29	71	66.4	36 2	US-09-451-067-55	Sequence 55, Appl
30	71	66.4	36 2	US-09-557-465D-6	Sequence 6, Appli
31	71	66.4	36 3	US-10-086-208-55	Sequence 55, Appl
32	71	66.4	56 1	US-08-450-257-7	Sequence 7, Appli
33	71	66.4	56 1	US-08-450-246-7	Sequence 7, Appli
34	71	66.4	56 1	US-08-450-098-7	Sequence 7, Appli
35	71	66.4	56 1	US-08-451-233-7	Sequence 7, Appli
36	71	66.4	56 1	US-08-450-236-7	Sequence 7, Appli
37	71	66.4	56 2	US-08-235-403-7	Sequence 7, Appli
38	71	66.4	72 1	US-07-910-867B-2	Sequence 2, Appli
39	71	66.4	72 1	US-08-893-853-1	Sequence 1, Appli
40	71	66.4	72 2	US-09-030-613-17	Sequence 17, Appl
41	71	66.4	72 2	US-09-113-921-1	Sequence 1, Appli
42	71	66.4	72 2	US-09-451-905-17	Sequence 15, Appl
43	71	66.4	72 2	US-09-561-366B-15	Sequence 10, Appl
44	71	66.4	72 2	US-09-347-504-10	Sequence 10, Appl
45	71	66.4	72 2	US-08-902-572-12	Sequence 12, Appl

## ALIGNMENTS

RESULT 1  
US-10-290-579A-219  
; Sequence 219, Application US/10290579A  
; Patent No. 6897301  
; GENERAL INFORMATION:  
; APPLICANT: Hahn, Beatrice  
; APPLICANT: Shaw, George  
; TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN  
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS TYPE 1  
; FILE REFERENCE: D6287D  
; CURRENT APPLICATION NUMBER: US/10/290.579A  
; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: US 09/184,418  
; FILING DATE: 1999-11-02  
; NUMBER OF SEQ ID NOS: 270  
; SEQ ID NO 219  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; OTHER INFORMATION: isolate=92RW009.6; gene=tat  
US-10-290-579A-219

Query Match 68.2%; Score 73; DB 2; Length 101;  
Best Local Similarity 65.0%; Pred. NO. 0.00052;  
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKRRRRRKPASADGHR 20  
Db 47 YGRKRRRRRNPSSSDHQ 66

RESULT 2  
US-09-475-515-86  
; Sequence 86, Application US/09475515A  
; Patent No. 6602705  
; GENERAL INFORMATION:  
; APPLICANT: BARNETT, Susan  
; APPLICANT: ZUR MEGEDE, Jan  
; APPLICANT: SRIVASTAVA, Indresh  
; APPLICANT: LIAN, Ying  
; APPLICANT: HARTOG, Karin  
; APPLICANT: LIU, Hong  
; APPLICANT: GREER, Catherine  
; APPLICANT: SELBY, Mark  
; APPLICANT: WALKER, Christopher  
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION  
; TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES



OTHER INFORMATION: SF162 protein  
US-09-475-515-90

Query Match 67.3%; Score 72; DB 2; Length 102;  
Best Local Similarity 65.0%; Pred. No. 0.00074;  
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRKPASADGHR 20  
| | | | | | | | | | : : :  
Db 47 YGRKKRRQRRRAPDPSEVHQ 66

RESULT 7  
US-08-450-257-48  
; Sequence 48, Application US/08450257  
; Patent No. 5652122  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,257  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-450-257-48

Query Match 66.4%; Score 71; DB 1; Length 26;

Best Local Similarity 65.0%; Pred. No. 0.00027;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 YGRKKRRQRRRKPASADGHR 20  
| | | | | | | | | | : : :  
Db 1 YGRKKRRQRRRPPGSGOTHQ 20

RESULT 8  
US-08-450-246-48  
; Sequence 48, Application US/08450246  
; Patent No. 5670617  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,246  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-450-246-48

Query Match 66.4%; Score 71; DB 1; Length 26;  
Best Local Similarity 65.0%; Pred. No. 0.00027;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRRKPASADGHR 20

us-10-814-109-2.ra1

Fri Aug 25 11:24:30 2006

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Db      1 YGRKKRQRRRPPQGSQTHQ 20
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RESULT 9
US-08-450-098-48
; Sequence 48, Application US/08450098
; Patent No. 5674980
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,098
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-450-098-48

Query Match      66.4%; Score 71; DB 1; Length 26;
Best Local Similarity 65.0%; Pred. No. 0.00027;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 YGRKKRQRRRPPQGSQTHQ 20
      |||||||
Db      1 YGRKKRQRRRPPQGSQTHQ 20
      |||||||
RESULT 11
US-08-450-236-48
; Sequence 48, Application US/08450236
; Patent No. 5804604
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,233
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-451-233-48

Query Match      66.4%; Score 71; DB 1; Length 26;
Best Local Similarity 65.0%; Pred. No. 0.00027;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 YGRKKRQRRRPPQGSQTHQ 20
      |||||||
Db      1 YGRKKRQRRRPPQGSQTHQ 20
      |||||||

```

GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOUM, James G.  
APPLICANT: FAWELL, Stephen E.  
APPLICANT: PEPINSKY, R. B.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,236  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-450-236-48

Query Match 66.4%; Score 71; DB 1; Length 26;  
Best Local Similarity 65.0%; Pred. No. 0.00027;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGRKKRQRRRKPSADGHR 20  
DB 1 YGRKKRQRRRKPSADGHR 20

RESULT 12  
US-08-235-403-48  
Sequence 48, Application US/08235403  
Patent No. 6316003  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOUM, James G.

GENERAL INFORMATION:  
APPLICANT: FAWELL, Stephen E.  
APPLICANT: PEPINSKY, R. B.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/235,403  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-235-403-48

Query Match 66.4%; Score 71; DB 2; Length 26;  
Best Local Similarity 65.0%; Pred. No. 0.00027;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGRKKRQRRRKPSADGHR 20  
DB 1 YGRKKRQRRRKPSADGHR 20

RESULT 13  
US-08-450-257-49  
Sequence 49, Application US/08450257  
Patent No. 5652122  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOUM, James G.  
APPLICANT: FAWELL, Stephen E.  
APPLICANT: PEPINSKY, R. B.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE

```
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,257
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-450-257-49

Query Match 66.4%; Score 71; DB 1; Length 35;
Best Local Similarity 65.0%; Pred. No. 0.00036;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKRRRRRRRRKPASADGHR 20
Db 10 YGKRRRRRRRRPPQGSQTHQ 29

RESULT 14
US-08-450-246-49
; Sequence 49, Application US/08450246
; Patent No. 5670617
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
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; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,246
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-450-246-49

Query Match 66.4%; Score 71; DB 1; Length 35;
Best Local Similarity 65.0%; Pred. No. 0.00036;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YGKRRRRRRRRKPASADGHR 20
Db 10 YGKRRRRRRRRPPQGSQTHQ 29

RESULT 15
US-08-450-098-49
; Sequence 49, Application US/08450098
; Patent No. 5674980
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,098
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-450-098-49

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Query Match      66.4%; Score 71; DB 1; Length 35;
Best Local Similarity 65.0%; Pred. No. 0.00036;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 YGRKKRRQRRRKPASADGHR 20
Db      10 YGRKKRRQRRRPPQGSQTHQ 29

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Search completed: August 24, 2006, 23:39:08  
Job time : 51 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2006, 23:28:36 ; Search time 196 Seconds  
(without alignments)  
46.655 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 107

Sequence: 1 YGRKRRRRRKPASADGHR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_8.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	20	9	Aed21152 SUDAPI-1/
2	80	74.8	101	9	Adx40278 HIV Tat p
3	78	72.9	100	9	Adx40269 HIV Tat p
4	78	72.9	101	9	Adx40367 HIV Tat p
5	78	72.9	101	9	Adx40406 HIV Tat p
6	78	72.9	101	9	Aeb10643 Clade C t
7	77	72.0	101	9	Adx40408 HIV Tat p
8	77	72.0	101	9	Adx40298 HIV Tat p
9	75	70.1	72	2	Aar10515 ARV tat g
10	75	70.1	100	9	Adx40365 HIV Tat p
11	75	70.1	101	9	Adx40316 HIV Tat p
12	75	70.1	101	9	Adx40407 HIV Tat p
13	75	70.1	101	9	Adx40319 HIV Tat p
14	75	70.1	102	9	Adx40285 HIV Tat p
15	75	70.1	1896	5	Aau84590 HIV Casse
16	75	70.1	5746	5	Aau84596 HIV compl
17	74	69.2	101	9	Adx40347 HIV Tat p
18	74	69.2	101	9	Adx40289 HIV Tat p
19	74	69.2	101	9	Adx40343 HIV Tat p
20	74	69.2	101	9	Adx40401 HIV Tat p
21	73	68.2	101	3	Aab69315 HIV-1 non
22	73	68.2	101	9	Adx40288 HIV Tat p
23	73	68.2	101	9	Adx40324 HIV Tat p

ALIGNMENTS

RESULT 1

AED21152  
ID AED21152 standard; peptide; 20 AA.

XX AC AED21152;

XX DT 01-DEC-2005 (first entry)

XX DE SUDAPI-1/ HIV Tat domain fusion peptide, TSUDAPI-1 SEQ ID NO: 2.

XX KW Protein interaction; therapeutic; cerebrovascular ischemia; cerebroprotective; vasotropic; hypoxia; ischemia; multiple sclerosis; neuroprotective; Huntingtons chorea; anticonvulsant; nootropic; parkinsons disease; antiparkinsonian; Alzheimers disease; hyperglycemia; antidiabetic; diabetes; trauma; tranquilizer; vulnery; epilepsy; grand mal seizure; muscle hypertonia; muscle relaxant; paralysis; muscular-gen.; asthma; antiasthmatic; cardiac arrest; cardiast; macular degeneration; ophthalmologic; psychiatric disorder; neuroleptic; schizophrenia; AIDS dementia complex; dementia; inflammation; antiinflammatory; pain; analgesic; opiate dependence; antiaddictive; cocaine addiction; alcoholism; antialcoholic; anorexia nervosa; anabolic; eating-disorders-gen.; Src-unique domain anchoring protein inhibitor.

XX KW Homo sapiens.

OS Human immunodeficiency virus.

XX FH Key Location/Qualifiers

FT Region 1. .11 /note= "HIV transduction domain (TAT)"

FT Region 12. .20 /note= "Src unique domain anchoring protein inhibitor 1"

FT FT

XX US2005222042-A1.

XX 06-OCT-2005.

XX PF 30-MAR-2004; 2004US-00814109.

XX PR 30-MAR-2004; 2004US-00814109.

XX PA (HOSP-) HOSPITAL FOR SICK CHILDREN RES INST.

XX PI Salter MW, Gingrich JR;

XX DR WPI; 2005-689427/71.

Adx40358 HIV Tat p  
Ady93250 HIV Tat p  
Adr46403 HIV Tat p  
Aau84593 HIV Casse  
Aab46680 HIV-1 Tat  
Aab46681 HIV-1 Tat  
Adx40266 HIV Tat p  
Aab69319 HIV-1 non  
Aab69322 HIV-1 non  
Aab69320 HIV-1 non  
Aab14224 HIV Tat S  
Aas37588 HIV-1 sub  
Aae37594 HIV-1 sub  
Aae37587 HIV-1 sub  
Ada16243 HIV-1 Tat  
Adx16230 HIV-1 Tat  
Adx40293 HIV Tat p  
Adx40287 HIV Tat p  
Adx40291 HIV Tat p  
Adx40286 HIV Tat p  
Adx40369 HIV Tat p  
Adx40277 HIV Tat p

XX Modifying N-methyl-D-aspartate receptor interaction with non-receptor  
PT tyrosine kinase Src in cells, comprises administering composition  
PT comprising Src-unique domains anchoring protein inhibitor to cells.  
XX  
XX Claim 13; SEQ ID NO 2; 32pp; English.  
PS  
XX The present invention provides a method for modifying N-methyl-D-  
CC aspartate receptor (NMDAR) interaction with non-receptor tyrosine kinase  
CC Src in cells. The method involves administering a composition including  
CC at least one Src-unique domain anchoring protein inhibitor (SUDAPI) to  
CC the cells, where modification ameliorates a disease or condition related  
CC to NMDAR signaling. Diseases or conditions ameliorated by the invention  
CC include stroke, hypoxia, ischemia, multiple sclerosis, Huntington's  
CC chorea, Parkinson's disease, Alzheimer's disease, hyperglycemia,  
CC diabetes, traumatic injury, epilepsy, grand mal seizures, spasticity,  
CC cerebral palsy, asthma, cardiac arrest, macular degeneration, mental  
CC diseases, schizophrenia, AIDS dementia complex, other dementias, AIDS  
CC wasting syndrome, inflammation, pain, opioid addiction, cocaine addiction,  
CC alcohol addiction and other conditions associated with substance abuse  
CC and anorexia. The present sequence is the SUDAPI-I/HIV Tat domain fusion  
CC peptide, TSUDAPI-I.  
XX  
XX Sequence 20 AA;  
XX  
XX Query Match 100.0%; Score 107; DB 9; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.6e-08;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YGRKKRRQRRKPPASADGHR 20  
DB 1 YGRKKRRQRRKPPASADGHR 20  
RESULT 2  
ADX40278  
ID ADX40278 standard; protein; 101 AA.  
XX  
XX ADX40278;  
XX  
XX 21-APR-2005 (first entry)  
XX HIV Tat protein #20.  
XX Immune stimulation; Tat.  
XX Human immunodeficiency virus.  
XX WO2005012502-A2.  
XX 10-FEB-2005.  
XX 29-MAR-2004; 2004WO-US009510.  
XX 28-MAR-2003; 2003US-0458026P.  
XX (EPIM-) EPIMUNE INC.  
XX Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;  
XX WPI; 2005-132661/14.  
XX Identifying a candidate peptide epitope, which induces a HLA class I CTL  
XX response comprises identifying variants of a peptide epitope 8-11 amino  
XX acids in length comprising primary anchor residues of the same HLA class  
XX I binding motif.  
XX Disclosure; Page 333-338; 458pp; English.  
XX The invention relates to a method of identifying a candidate peptide  
XX epitope which induces an HLA class I CTL response against variants of the  
XX peptide epitope, comprising identifying, from a particular antigen of an  
XX infectious agent, variants of a peptide epitope comprising primary anchor  
XX residues of the same HLA class I binding motif. The method is useful for  
XX identifying a candidate peptide epitope, which induces an HLA class I CTL  
XX response against variants of the peptide epitope. This sequence  
XX represents an HIV Tat protein used in the scope of the invention.  
XX  
XX Sequence 101 AA;  
XX  
XX Query Match 74.8%; Score 80; DB 9; Length 101;  
XX Best Local Similarity 70.0%; Pred. No. 0.00062;  
XX Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 YGRKKRRQRRKPPASADGHR 20  
DB 47 YGRKKRRQRRRSPQSSSEAHQ 66  
RESULT 3  
ADX40269  
ID ADX40269 standard; protein; 100 AA.  
XX  
XX ADX40269;  
XX  
XX 21-APR-2005 (first entry)  
XX HIV Tat protein #11.  
XX Immune stimulation; Tat.  
XX Human immunodeficiency virus.  
XX WO2005012502-A2.  
XX 10-FEB-2005.  
XX 29-MAR-2004; 2004WO-US009510.  
XX 28-MAR-2003; 2003US-0458026P.  
XX (EPIM-) EPIMUNE INC.  
XX Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;  
XX WPI; 2005-132661/14.  
XX Identifying a candidate peptide epitope, which induces a HLA class I CTL  
XX response comprises identifying variants of a peptide epitope 8-11 amino  
XX acids in length comprising primary anchor residues of the same HLA class  
XX I binding motif.  
XX Disclosure; Page 332-338; 458pp; English.  
XX The invention relates to a method of identifying a candidate peptide  
XX epitope which induces an HLA class I CTL response against variants of the  
XX peptide epitope, comprising identifying, from a particular antigen of an  
XX infectious agent, variants of a peptide epitope comprising primary anchor  
XX residues of the same HLA class I binding motif. The method is useful for  
XX identifying a candidate peptide epitope, which induces an HLA class I CTL  
XX response against variants of the peptide epitope. This sequence  
XX represents an HIV Tat protein used in the scope of the invention.  
XX  
XX Sequence 100 AA;  
XX  
XX Query Match 72.9%; Score 78; DB 9; Length 100;  
XX Best Local Similarity 70.0%; Pred. No. 0.0012;  
XX Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 YGRKKRRQRRKPPASADGHR 20  
DB 47 YGRKKRRQRRRPPSSSEHQ 66  
RESULT 4  
ADX40367

XX Modifying N-methyl-D-aspartate receptor interaction with non-receptor  
PT tyrosine kinase Src in cells, comprises administering composition  
PT comprising Src-unique domains anchoring protein inhibitor to cells.  
XX  
XX Claim 13; SEQ ID NO 2; 32pp; English.  
PS  
XX The present invention provides a method for modifying N-methyl-D-  
CC aspartate receptor (NMDAR) interaction with non-receptor tyrosine kinase  
CC Src in cells. The method involves administering a composition including  
CC at least one Src-unique domain anchoring protein inhibitor (SUDAPI) to  
CC the cells, where modification ameliorates a disease or condition related  
CC to NMDAR signaling. Diseases or conditions ameliorated by the invention  
CC include stroke, hypoxia, ischemia, multiple sclerosis, Huntington's  
CC chorea, Parkinson's disease, Alzheimer's disease, hyperglycemia,  
CC diabetes, traumatic injury, epilepsy, grand mal seizures, spasticity,  
CC cerebral palsy, asthma, cardiac arrest, macular degeneration, mental  
CC diseases, schizophrenia, AIDS dementia complex, other dementias, AIDS  
CC wasting syndrome, inflammation, pain, opioid addiction, cocaine addiction,  
CC alcohol addiction and other conditions associated with substance abuse  
CC and anorexia. The present sequence is the SUDAPI-I/HIV Tat domain fusion  
CC peptide, TSUDAPI-I.  
XX  
XX Sequence 20 AA;  
XX  
XX Query Match 100.0%; Score 107; DB 9; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.6e-08;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YGRKKRRQRRKPPASADGHR 20  
DB 1 YGRKKRRQRRKPPASADGHR 20  
RESULT 2  
ADX40278  
ID ADX40278 standard; protein; 101 AA.  
XX  
XX ADX40278;  
XX  
XX 21-APR-2005 (first entry)  
XX HIV Tat protein #20.  
XX Immune stimulation; Tat.  
XX Human immunodeficiency virus.  
XX WO2005012502-A2.  
XX 10-FEB-2005.  
XX 29-MAR-2004; 2004WO-US009510.  
XX 28-MAR-2003; 2003US-0458026P.  
XX (EPIM-) EPIMUNE INC.  
XX Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;  
XX WPI; 2005-132661/14.  
XX Identifying a candidate peptide epitope, which induces a HLA class I CTL  
XX response comprises identifying variants of a peptide epitope 8-11 amino  
XX acids in length comprising primary anchor residues of the same HLA class  
XX I binding motif.  
XX Disclosure; Page 333-338; 458pp; English.  
XX The invention relates to a method of identifying a candidate peptide  
XX epitope which induces an HLA class I CTL response against variants of the  
XX peptide epitope, comprising identifying, from a particular antigen of an  
XX infectious agent, variants of a peptide epitope comprising primary anchor

ID ADX40367 standard; protein; 101 AA.  
XX AC ADX40367;  
XX DT 21-APR-2005 (first entry)  
XX DE HIV Tat protein #109.  
XX KW Immune stimulation; Tat.  
XX OS Human immunodeficiency virus.  
XX PN WO2005012502-A2.  
XX PD 10-FEB-2005.  
XX PF 29-MAR-2004; 2004WO-US009510.  
XX PR 28-MAR-2003; 2003US-0458026P.  
XX PA (EPIM-) EPIIMMUNE INC.  
PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;  
XX WPI; 2005-132661/14.  
XX Identifying a candidate peptide epitope, which induces a HLA class I CTL response comprises identifying variants of a peptide epitope 8-11 amino acids in length comprising primary anchor residues of the same HLA class I binding motif.  
PS Disclosure: Page 334-340; 458pp; English.  
XX The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HIV Tat protein used in the scope of the invention.  
XX Sequence 101 AA;  
XX Query Match 72.9%; Score 78; DB 9; Length 101;  
XX Best Local Similarity 70.0%; Pred. No. 0.0012;  
XX Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 YGRKKRRQRRRKPSADGHR 20  
DB 47 YGRKKRRQRRRKPSADGHR 66  
RESULT 5  
ID ADX40406 standard; protein; 101 AA.  
XX AC ADX40406;  
XX DT 21-APR-2005 (first entry)  
XX DE HIV Tat protein #148.  
XX KW Immune stimulation; Tat.  
XX OS Human immunodeficiency virus.  
XX PN WO2005012502-A2.  
XX PD 10-FEB-2005.  
XX PR 29-MAR-2004; 2004WO-US009510.  
XX

PR 28-MAR-2003; 2003US-0458026P.  
XX (EPIM-) EPIIMMUNE INC.  
XX PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;  
XX WPI; 2005-132661/14.  
XX Identifying a candidate peptide epitope, which induces a HLA class I CTL response comprises identifying variants of a peptide epitope 8-11 amino acids in length comprising primary anchor residues of the same HLA class I binding motif.  
XX PS Disclosure: Page 335-340; 458pp; English.  
XX The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HIV Tat protein used in the scope of the invention.  
XX Sequence 101 AA;  
XX Query Match 72.9%; Score 78; DB 9; Length 101;  
XX Best Local Similarity 70.0%; Pred. No. 0.0012;  
XX Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 YGRKKRRQRRRKPSADGHR 20  
DB 47 YGRKKRRQRRRKPSADGHR 66  
RESULT 6  
ID AEB10643 standard; protein; 101 AA.  
XX AC AEB10643;  
XX DT 25-AUG-2005 (first entry)  
XX DE Clade C tat protein, Ctat.mrca, SEQ ID NO: 110.  
XX KW Immune stimulation; diagnosis; gene therapy; viral infection; virucide; infection; HIV infection; anti-hiv; tat protein.  
XX OS Synthetic.  
XX PN US2005137387-A1.  
XX PD 23-JUN-2005.  
XX PF 17-FEB-2004; 2004US-00780507.  
XX PR 18-FEB-2000; 2000US-0183659P.  
XX PR 16-FEB-2001; 2001US-00204204.  
XX PR 16-FEB-2001; 2001WO-US005288.  
XX PR 14-FEB-2003; 2003US-0447586P.  
XX PA (UNIW ) UNIV WASHINGTON OFFICE TECHNOLOGY TRANSF.  
XX PI Mullins JT, Rodrigo AG, Learn GH, Li F, Nickle DC, Jensen MA;  
XX WPI; 2005-444181/45.  
XX DR N-ESDB; AEB10617.  
XX New isolated ancestral or COT viral nucleic acid and amino acid sequences that are determined founder sequences of a highly diverse viral strain, useful for diagnosing, preventing or treating viral (e.g. HIV) infection.  
XX Claim 11; SEQ ID NO 110; 201pp; English.  
XX



XX Human T-cell leukaemia virus; HTLV-III; acquired immune deficiency; AIDS;  
KW transactivation; LAV.  
XX Human immunodeficiency virus.  
XX US4981790-A.  
XX 01-JAN-1991.  
XX 06-DEC-1985; 85US-00806263.  
XX 25-MAY-1984; 84US-00614297.  
XX (DAND ) DANA FARBER CANCER INST INC.  
XX Haseltine WA, Rosen CA, Sodroeki JG, Goh WC;  
XX WPI; 1991-029335/04.  
DR N-PSDB; AAQ10398.  
XX Stable cell lines contg. HTLV-III-LAV TAT-III gene - formed by  
PT transfecting cell and culturing used to study or detect infection.  
XX Disclosure; Fig 7; 16pp; English.  
XX The sequence is that of the tatIII gene product, which regulates gene  
CC expression directed by the HTLV-II/LAV long terminal repeat. See also  
CC AAR10511-14. (Updated on 10-MAR-2003 to add missing OS field.) (Updated  
CC on 25-MAR-2003 to correct PA field.)  
XX Sequence 72 AA;  
SQ  
Query Match 70.1%; Score 75; DB 2; Length 72;  
Best Local Similarity 70.0%; Pred. No. 0.0024; 4; Indels 0; Gaps 0;  
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 YGRKKRRQRRRKPASADGHR 20  
|||||  
Db 47 YGRKKRRQRRRAPRSSQTHQ 66  
RESULT 10  
ADX40365  
ID ADX40365 standard; protein; 100 AA.  
XX  
AC ADX40365;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE HIV Tat protein #107.  
XX  
KW Immune stimulation; Tat.  
XX  
OS Human immunodeficiency virus.  
XX  
PN WO2005012502-A2.  
XX  
PD 10-FEB-2005.  
XX  
XX 29-MAR-2004; 2004WO-US009510.  
XX  
XX 28-MAR-2003; 2003US-0458026P.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;  
PI WPI; 2005-132661/14.  
XX  
XX Identifying a candidate peptide epitope, which induces a HLA class I CTL  
PT response comprises identifying variants of a peptide epitope 8-11 amino  
PT acids in length comprising primary anchor residues of the same HLA class

PT I binding motif.  
XX  
PS Disclosure; Page 334-340; 458pp; English.  
XX  
XX The invention relates to a method of identifying a candidate peptide  
CC epitope which induces an HLA class I CTL response against variants of the  
CC peptide epitope, comprising identifying, from a particular antigen of an  
CC infectious agent, variants of a peptide epitope comprising primary anchor  
CC residues of the same HLA class I binding motif. The method is useful for  
CC identifying a candidate peptide epitope, which induces an HLA class I CTL  
CC response against variants of the peptide epitope. This sequence  
CC represents an HIV Tat protein used in the scope of the invention.  
XX  
SQ Sequence 100 AA;  
Query Match 70.1%; Score 75; DB 9; Length 100;  
Best Local Similarity 70.0%; Pred. No. 0.0033;  
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 YGRKKRRQRRRKPASADGHR 20  
|||||  
Db 46 YGRKKRRQRRRAPQSSKDQ 65  
RESULT 11  
ADX40316  
ID ADX40316 standard; protein; 101 AA.  
XX  
AC ADX40316;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE HIV Tat protein #58.  
XX  
KW Immune stimulation; Tat.  
XX  
OS Human immunodeficiency virus.  
XX  
PN WO2005012502-A2.  
XX  
PD 10-FEB-2005.  
XX  
XX 29-MAR-2004; 2004WO-US009510.  
XX  
XX 28-MAR-2003; 2003US-0458026P.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;  
PI WPI; 2005-132661/14.  
XX  
XX Identifying a candidate peptide epitope, which induces a HLA class I CTL  
PT response comprises identifying variants of a peptide epitope 8-11 amino  
PT acids in length comprising primary anchor residues of the same HLA class  
PT I binding motif.  
XX  
PS Disclosure; Page 333-339; 458pp; English.  
XX  
XX The invention relates to a method of identifying a candidate peptide  
CC epitope which induces an HLA class I CTL response against variants of the  
CC peptide epitope, comprising identifying, from a particular antigen of an  
CC infectious agent, variants of a peptide epitope comprising primary anchor  
CC residues of the same HLA class I binding motif. The method is useful for  
CC identifying a candidate peptide epitope, which induces an HLA class I CTL  
CC response against variants of the peptide epitope. This sequence  
CC represents an HIV Tat protein used in the scope of the invention.  
XX  
SQ Sequence 101 AA;  
Query Match 70.1%; Score 75; DB 9; Length 101;  
Best Local Similarity 70.0%; Pred. No. 0.0033;  
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;



PT acids in length comprising primary anchor residues of the same HLA class  
 PT I binding motif.

XX Disclosure; Page 333-338; 458pp; English.

XX The invention relates to a method of identifying a candidate peptide  
 CC epitope which induces an HLA class I CTL response against variants of the  
 CC peptide epitope, comprising identifying, from a particular antigen of an  
 CC infectious agent, variants of a peptide epitope comprising primary anchor  
 CC residues of the same HLA class I binding motif. The method is useful for  
 CC identifying a candidate peptide epitope, which induces an HLA class I CTL  
 CC response against variants of the peptide epitope. This sequence  
 CC represents an HIV Tat protein used in the scope of the invention.

XX Sequence 102 AA;

Query Match 70.1%; Score 75; DB 9; Length 102;  
 Best Local Similarity 65.0%; Pred. No. 0.0034;  
 Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPASADGHR 20

Db 47 YGRKKRRQRRSPSSSENHQ 66

RESULT 15

AAU84590

ID AAU84590 standard; protein; 1896 AA.

XX AC AAU84590;

DT 08-MAY-2002 (first entry)

XX HIV Cassette A1 protein.

XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;

XX viral infection; human immunodeficiency virus; melanoma;

XX bacterial infection; Salmonella; Legionella; parasitic infection;

XX Trypanosoma; Toxoplasma; Giardia.

XX Human immunodeficiency virus 1.

OS Synthetic.

XX WO200190197-A1.

XX 29-NOV-2001.

XX 25-MAY-2001; 2001WO-AU000622.

XX 26-MAY-2000; 2000AU-00007761.

XX (AUSU ) UNIV AUSTRALIAN NAT.

XX Thomson SA, Ramshaw IA;

XX WPI; 2002-147575/19.

DR N-PSDB; ABK36429.

XX New synthetic polypeptides having several different segments of at least  
 PT one parent polypeptide linked together differently compared to the  
 PT linkage in the parent polypeptide, for inducing immune response against a  
 PT pathogen or cancer.

XX Example 1; SEQ ID NO 393; 364pp; English.

PS The invention relates to a new synthetic polypeptide (I) comprising  
 CC several different segments of at least one parent polypeptide linked  
 CC together in a different relationship relative to their linkage in the  
 CC parent polypeptide to impede, abrogate or otherwise alter at least one  
 CC function associated with the parent polypeptide and for inducing an  
 CC immune response against a pathogen or cancer. Also included are a  
 CC synthetic polynucleotide encoding and a computer system for designing the  
 CC synthetic polypeptides. The synthetic polypeptides and polynucleotides

CC are referred to as a Savine. The synthetic polypeptide is useful for  
 CC modulating immune responses preferably directed against a pathogen or a  
 CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head  
 CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,  
 CC oesophagus, brain, testicle, uterus); as potentiating agents.  
 CC Compositions comprising the polypeptide may be used in the treatment or  
 CC prophylaxis against viral (such as infections caused by HIV (human  
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis  
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial  
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,  
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic  
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,  
 CC Trypanosoma, toxoplasma and Giardia) infections. The present sequence is  
 CC a cassette protein consisting of several peptides derived from a parent  
 CC protein. One or more cassettes are used to construct a savine of the  
 CC invention

XX Sequence 1896 AA;

Query Match 70.1%; Score 75; DB 5; Length 1896;  
 Best Local Similarity 70.0%; Pred. No. 0.05;  
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGRKKRRQRRKPASADGHR 20

Db 186 YGRKKRRQRRAPQSSKDQ 205

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